

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 11, 2004, 09:14:02 ; Search time 21 seconds
(without alignments)
41.225 Million cell updates/sec

Title: US-09-734-628-1

Perfect score: 65

Sequence: 1 CDCRGDCFC 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 78.*

1: PIR1.*

2: PIR2.*

3: PIR3.*

4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	67.7	577	2 B37057	integrin beta-6 ch
2	44	67.7	788	2 A37057	integrin beta-6 ch
3	43	66.2	1076	2 T26044	hypothetical prote
4	43	66.2	1627	2 S65464	pregnancy-associat
5	43	66.2	4753	1 A47437	LDL-receptor-relat
6	42.5	65.4	48	2 S29216	neurotoxin Tx2 - s
7	42.5	65.4	49	2 S29215	neurotoxin Tx2 - s
8	42.5	65.4	53	2 S29214	neurotoxin Tx2 - s
9	41	63.1	69	2 A55011	metallothionein-li
10	41	63.1	458	2 A84306	hypothetical prote
11	41	63.1	736	2 T06757	hypothetical prote
12	41	63.1	3672	2 T23433	hypothetical prote
13	41	63.1	3704	2 T37316	probable laminin a
14	40	61.5	195	1 TVVPA	small T antigen -
15	40	61.5	195	2 S22562	small T antigen -
16	40	61.5	313	2 S44208	extracellular matr
17	40	61.5	421	1 TVVPM	middle T antigen -
18	40	61.5	421	2 S22561	middle T antigen -
19	40	61.5	440	1 TVVPM	middle T antigen -
20	39.5	60.8	246	2 A24609	acidic epidiolymal
21	39	60.0	30	2 JX0057	trypsin inhibitor
22	39	60.0	32	2 A05076	metallothionein -
23	39	60.0	50	2 T38209	probable metalloth
24	39	60.0	60	2 S30567	metallothionein -
25	39	60.0	60	2 JC2420	metallothionein -
26	39	60.0	61	1 SMO20	metallothionein II
27	39	60.0	61	2 S00808	metallothionein Ia
28	39	60.0	61	2 S00810	metallothionein Ic
29	39	60.0	61	2 S00809	metallothionein Ib

30	39	60.0	61	2 I46602	metallothionein -
31	39	60.0	68	2 S44392	metallothionein 3
32	39	60.0	656	2 JC2005	integrin beta-5 ch
33	39	60.0	799	2 A38308	integrin beta-5 ch
34	39	60.0	850	2 S56015	gastric mucin MUC5
35	39	60.0	1182	2 I48378	hairless protein -
36	39	60.0	1291	2 T21694	hypothetical prote
37	39	60.0	1321	2 JE0352	mucin MUC5B, trach
38	39	60.0	1373	2 JE0095	gastric mucin MUC5
39	39	60.0	1513	2 A54895	mucin 2, intestina
40	39	60.0	3020	2 A43932	mucin 2 precursor
41	38.5	59.2	788	2 I51530	integrin beta-3 su
42	38	58.5	40	1 SMFF	metallothionein Mc
43	38	58.5	40	2 B61194	metallothionein Mc
44	38	58.5	60	2 S31723	metallothionein -
45	38	58.5	60	2 B27490	metallothionein B

ALIGNMENTS

RESULT 1

B37057 integrin beta-6 chain - guinea pig (fragment)

C:Species: Cavia porcellus (guinea pig)

C>Date: 15-Feb-1991 #sequence_revision 13-Sep-1991 #text_change 20-Aug-1999

C:Accession: B37057

R:Sheppard, D.; Rozzo, C.; Starr, L.; Quaranta, V.; Erle, D.J.; Pytela, R.

J. Biol. Chem. 265, 11502-11507, 1990

A:Title: Complete amino acid sequence of a novel integrin beta subunit (beta6) identified

A:Reference number: A37057; MUID:90307659; PMID:2365683

A:Accession: B37057

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-577 <SHE>

A:Cross-references: GB:M35197; GB:J05522; NID:g191277; PIDN:AAA37043.1; PID:g553845

A>Note: the authors translated the codon AAA for residue 88 as Asn, AAC for residue 97 as

as Pro, ACG for residue 355 as Met, GAG for residue 363 as Thr, ACC for residue 364 as Al

Gly

C:Superfamily: integrin beta chain; laminin-type EGF-like homology

C:Keywords: cell adhesion; cytoskeleton; transmembrane protein

Query Match 67.7%; Score 44; DB 2; Length 577;

Best Local Similarity 66.7%; Pred. No. 28;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CDCRGDCFC 9

Db 370 CSGRGDCYC 378

RESULT 2

A37057

integrin beta-6 chain - human

C:Species: Homo sapiens (man)

C>Date: 15-Feb-1991 #sequence_revision 13-Sep-1991 #text_change 19-Jan-2001

C:Accession: A37057; I69201

R:Sheppard, D.; Rozzo, C.; Starr, L.; Quaranta, V.; Erle, D.J.; Pytela, R.

J. Biol. Chem. 265, 11502-11507, 1990

A:Title: Complete amino acid sequence of a novel integrin beta subunit (beta6) identified

A:Reference number: A37057; MUID:90307659; PMID:2365683

A:Accession: A37057

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-788 <SHE>

A:Cross-references: GB:M35198; GB:J05522; NID:g186506; PIDN:AAA36122.1; PID:g186507

R:Jiang, W.M.; Jenkins, D.; Yuan, Q.; Leung, E.; Choo, K.H.; Watson, J.D.; Krissansen, G.

Int. Immunol. 4, 1031-1040, 1992

A:Title: The gene organization of the human beta 7 subunit, the common beta subunit of t

A:Reference number: I54749; MUID:93002753; PMID:1382574

A:Accession: I69201

A>Status: preliminary

A:Molecule type: DNA

A:Keywords: translated from GB/EMBL/DDBJ

A;Residues: 116-157, R', 159-197 <JTA>
A;Cross-references: GB:S49380; NID:G257588; PIDN:ABE23690.1; PID:G257589
A;Gene: GDB:ITGB6
C;Genetics:
A;Cross-references: GDB:131392; OMIM:147558
A;Map position: 2pter-2qter
C;Superfamily: integrin beta chain; laminin-type EGF-like homology
F;Keywords: blocked amino end; cell adhesion; cytoskeleton; glycoprotein; lipoprotein; #
F;708-730/Domain: transmembrane #status predicted <TRM>
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;7/Binding site: palmitate (Cys) (covalent) #status predicted
F;16,48,97,260,387,396,463,471/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 67.7%; Score 44; DB 2; Length 788;
Best Local Similarity 66.7%; Pred. No. 35;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 CDCRGDCFC 9
DB 511 CSGRGDCYC 519
RESULT 3
T26044
Hypothetical protein W01C8.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T26044
R;Nhan, M.
submitted to the EMBL Data Library, November 1995.
A;Description: The sequence of C. elegans cosmid W01C8.
A;Reference number: Z20142
A;Accession: T26044
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-1076 <NHA>
A;Cross-references: EMBL:U41508; PIDN:AAA82623.1; CESP:W01C8.3
C;Genetics:
A;Gene: CESP:W01C8.3
A;Introns: 59/3; 92/2; 157/3; 189/3; 220/2; 251/3; 275/2; 319/1; 374/3; 407/2
Query Match 66.2%; Score 43; DB 2; Length 1076;
Best Local Similarity 85.7%; Pred. No. 82;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CDCRGDC 7
DB 276 CGCRGDC 282
RESULT 4
S65464
pregnancy-associated plasma protein A precursor - human
N;Alternate names: PAP-A
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1996 #sequence_revision 22-Nov-1996 #text_change 05-Nov-1999
C;Accession: S65464; S65463; A54220; I38097
R;Haaning, J.; Oxvig, C.; Overgaard, M.T.; Ebbesen, P.; Kristensen, T.; Sottrup-Jensen,
Eur. J. Biochem. 237, 159-163, 1996
A;Description: Complete cDNA sequence of the preproform of human pregnancy-associated p
A;Reference number: S65464
A;Accession: S65464
A;Molecule type: mRNA
A;Residues: 1-1627 <HA>
A;Cross-references: EMBL:U28727; NID:g1142969; PIDN:AAC50543.1; PID:g1142970
R;Haaning, J.; Oxvig, C.; Overgaard, M.T.; Ebbesen, P.; Kristensen, T.; Sottrup-Jensen,
Eur. J. Biochem. 237, 159-163, 1996
A;Title: Complete cDNA sequence of the preproform of human pregnancy-associated plasma p
A;Reference number: S65463; MUID:96203921; PMID:8620868
A;Accession: S65463
A;Molecule type: mRNA
A;Residues: 1-102 <HAW>
A;Cross-references: EMBL:U28727

A;Note: the authors translated the codon CGA for residue 101 as Thr
R;Kristensen, T.; Oxvig, C.; Sand, O.; Moller, N.P.H.; Sottrup-Jensen, L.
Biochemistry 33, 1592-1598, 1994
A;Title: Amino acid sequence of human pregnancy-associated plasma protein-A derived from
A;Reference number: A54220; MUID:94146014; PMID:7508748
A;Accession: A54220
A;Molecule type: mRNA
A;Residues: 77-1627 <KRI>
A;Cross-references: GB:X68280; NID:g394649; PIDN:CAA48341.1; PID:g394650
R;Oxvig, C.; Sand, O.; Kristensen, T.; Gleich, G.J.; Sottrup-Jensen, L.
J. Biol. Chem. 268, 12243-12246, 1993
A;Title: Circulating human pregnancy-associated plasma protein-A is disulfide-bridged to
A;Reference number: I38097; MUID:93286045; PMID:7683339
A;Accession: I38097
A;Status: translated from GB/EMBL/DBDJ
A;Molecule type: mRNA
A;Residues: 77-1627 <RES>
A;Cross-references: EMBL:X68280; NID:g394649; PIDN:CAA48341.1; PID:g394650
C;Genetics:
A;Gene: GDB:PAPPA
A;Cross-references: GDB:134729; OMIM:176385
A;Map position: 9q33.1-9q33.1
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-80/Domain: propeptide #status predicted <PRO>
F;81-1627/Product: pregnancy-associated plasma protein A #status predicted <MAT>
Query Match 66.2%; Score 43; DB 2; Length 1627;
Best Local Similarity 66.7%; Pred. No. 85;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 CDCRGDCFC 9
DB 1600 CDLQGDCCAC 1608
RESULT 5
A47437
LDL-receptor-related protein - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 18-Aug-2000
C;Accession: A47437; S27801; T21547
R;Yochem, J.; Greenwald, I.
Proc. Natl. Acad. Sci. U.S.A. 90, 4572-4576, 1993
A;Title: A gene for a low density lipoprotein receptor-related protein in the nematode C
A;Reference number: A47437; MUID:93281621; PMID:8506301
A;Accession: A47437
A;Molecule type: DNA
A;Residues: 1-4753 <YOC>
A;Cross-references: GB:M96150; NID:g156359; PIDN:AAA28105.1; PID:g156360
A;Note: nucleotide sequence not given; translation not complete in this paper
R;Yochem, J.; Greenwald, I.
submitted to the EMBL Data Library, July 1992
A;Description: A gene for an LDL receptor-related protein (LPR) in the nematode C.elegans
A;Reference number: S27801
A;Accession: S27801
A;Molecule type: DNA
A;Residues: 1-4753 <YO2>
A;Cross-references: EMBL:M96150; NID:g156359; PIDN:AAA28105.1; PID:g156360
R;Wilkinson, J.
submitted to the EMBL Data Library, June 1996
A;Reference number: Z19439
A;Accession: T21547
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-4753 <WIL>
A;Cross-references: EMBL:Z73907; PIDN:CAA98124.1; GSPDB:GN00019; CESP:F29D11.1
A;Experimental source: clone P29D11
C;Genetics:
A;Gene: LPR
A;Map position: 1
A;Introns: 31/1; 88/1; 132/1; 172/3; 219/1; 298/1; 463/2; 526/2; 585/3; 780/2; 874/2; 975
15/1
C;Superfamily: alpha-2-macroglobulin receptor; EGF homology; LDL receptor ligand-binding

C;Keywords: tandem repeat; transmembrane protein
F;53-87/Domain: LDL receptor ligand-binding repeat homology <LDL1>
F;92-131/Domain: LDL receptor ligand-binding repeat homology <LDL2>
F;138-175/Domain: LDL receptor ligand-binding repeat homology <LDL3>
F;182-218/Domain: LDL receptor ligand-binding repeat homology <LDL4>
F;223-257/Domain: LDL receptor ligand-binding repeat homology <LDL5>
F;262-297/Domain: LDL receptor ligand-binding repeat homology <LDL6>
F;302-336/Domain: EGF homology <EGF1>
F;1054-1095/Domain: LDL receptor ligand-binding repeat homology <LDL7>
F;1101-1138/Domain: LDL receptor ligand-binding repeat homology <LDL8>
F;1146-1182/Domain: LDL receptor ligand-binding repeat homology <LDL9>
F;1187-1223/Domain: LDL receptor ligand-binding repeat homology <LDL10>
F;1228-1263/Domain: LDL receptor ligand-binding repeat homology <LDL11>
F;1270-1307/Domain: LDL receptor ligand-binding repeat homology <LDL12>
F;1313-1350/Domain: LDL receptor ligand-binding repeat homology <LDL13>
F;1359-1396/Domain: LDL receptor ligand-binding repeat homology <LDL14>
F;1441-1475/Domain: EGF homology <EGF>
F;1611-1654/Domain: LDL receptor WYTD-containing repeat homology <YW33>
F;2792-2829/Domain: LDL receptor ligand-binding repeat homology <LDL5>
F;2834-2868/Domain: LDL receptor ligand-binding repeat homology <LDL16>
F;2874-2912/Domain: LDL receptor ligand-binding repeat homology <LDL17>
F;2919-2956/Domain: LDL receptor ligand-binding repeat homology <LDL18>
F;2961-2997/Domain: LDL receptor ligand-binding repeat homology <LDL19>
F;3006-3044/Domain: LDL receptor ligand-binding repeat homology <LDL20>
F;3049-3093/Domain: LDL receptor ligand-binding repeat homology <LDL21>
F;3100-3135/Domain: LDL receptor ligand-binding repeat homology <LDL22>
F;3140-3174/Domain: LDL receptor ligand-binding repeat homology <LDL23>
F;3187-3222/Domain: LDL receptor ligand-binding repeat homology <LDL24>
F;3586-3623/Domain: EGF homology <EGX1>
F;3627-3666/Domain: LDL receptor ligand-binding repeat homology <LDL25>
F;3671-3705/Domain: LDL receptor ligand-binding repeat homology <LDL26>
F;3709-3746/Domain: LDL receptor ligand-binding repeat homology <LDL27>
F;3753-3788/Domain: LDL receptor ligand-binding repeat homology <LDL28>
F;3793-3830/Domain: LDL receptor ligand-binding repeat homology <LDL29>
F;3833-3871/Domain: LDL receptor ligand-binding repeat homology <LDL30>
F;3878-3912/Domain: LDL receptor ligand-binding repeat homology <LDL31>
F;3917-3951/Domain: LDL receptor ligand-binding repeat homology <LDL32>
F;3959-3995/Domain: LDL receptor ligand-binding repeat homology <LDL33>
F;4000-4040/Domain: LDL receptor ligand-binding repeat homology <LDL34>
F;4049-4083/Domain: LDL receptor ligand-binding repeat homology <LDL35>
F;4092-4130/Domain: EGF homology <EGF2>
F;4343-4386/Domain: LDL receptor WYTD-containing repeat homology <YW38>

Query Match 66.2%; Score 43; DB 1; Length 4753;
Best Local Similarity 75.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CDCRGDCFC 8
Db 361 CSCIIGDCFC 368

RESULT 6
S29216
neurotoxin Tx2 - spider (Phoneutria nigriventer)
C;Species: Phoneutria nigriventer
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 07-May-1999
C;Accession: S29216
R;do Nascimento Cordeiro, M.; Ribeiro Diniz, C.; do Carmo Valentim, A.; von Eickstedt, V
FEBS Lett. 310, 153-156, 1992
A;Title: The purification and amino acid sequences of four Tx2 neurotoxins from the venom
A;Reference number: S29214; MUID:93011905; PMID:1397265
A;Accession: S29216
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-48 <COR>
C;Superfamily: curatatoxin

Query Match 65.4%; Score 42.5; DB 2; Length 48;
Best Local Similarity 58.3%; Pred. No. 7.2;
Matches 7; Conservative 1; Mismatches 1; Indels 3; Gaps 1;

Qy 1 CDC---RGDCFC 9
Db 14 CDCGGERGECVC 25

RESULT 9
A55011
metallothionein-like protein YOR031w - yeast (Saccharomyces cerevisiae)
C;Alternate names: protein O3675
C;Species: Saccharomyces cerevisiae
C;Date: 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change 19-Apr-2002
C;Accession: A55011; S66897
R;Culotta, V.C.; Howard, W.R.; Liu, X.F.
J. Biol. Chem. 269, 25295-25302, 1994
A;Title: CRS5 encodes a metallothionein-like protein in Saccharomyces cerevisiae.

Db 14 CDCGGERGECVC 25

RESULT 7

S29215
neurotoxin Tx2 - spider (Phoneutria nigriventer)

C;Species: Phoneutria nigriventer
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 15-Oct-1999
C;Accession: S29215; B39305
R;do Nascimento Cordeiro, M.; Ribeiro Diniz, C.; do Carmo Valentim, A.; von Eickstedt, V
FEBS Lett. 310, 153-156, 1992
A;Title: The purification and amino acid sequences of four Tx2 neurotoxins from the venom
A;Reference number: S29214; MUID:93011905; PMID:1397265
A;Accession: S29215
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-49 <COR>
R;Rezende Jr., L.; Cordeiro, M.N.; Oliveira, E.B.; Diniz, C.R.
Toxicol 29, 1225-1233, 1991
A;Title: Isolation of neurotoxic peptides from the venom of the 'armed' spider Phoneutria

A;Reference number: A39305; MUID:92196803; PMID:1801316

A;Accession: B39305

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <REZ>

C;Superfamily: curatatoxin

C;Keywords: neurotoxin; venom

Query Match 65.4%; Score 42.5; DB 2; Length 49;
Best Local Similarity 58.3%; Pred. No. 7.3;
Matches 7; Conservative 1; Mismatches 1; Indels 3; Gaps 1;

Qy 1 CDC---RGDCFC 9

Db 14 CDCGGERGECVC 25

RESULT 8

S29214
neurotoxin Tx2 - spider (Phoneutria nigriventer)

C;Species: Phoneutria nigriventer
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 07-May-1999
C;Accession: S29214
R;do Nascimento Cordeiro, M.; Ribeiro Diniz, C.; do Carmo Valentim, A.; von Eickstedt, V
FEBS Lett. 310, 153-156, 1992
A;Title: The purification and amino acid sequences of four Tx2 neurotoxins from the venom
A;Reference number: S29214; MUID:93011905; PMID:1397265
A;Accession: S29214
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-53 <COR>
C;Superfamily: curatatoxin

Query Match 65.4%; Score 42.5; DB 2; Length 53;
Best Local Similarity 58.3%; Pred. No. 7.7;
Matches 7; Conservative 1; Mismatches 1; Indels 3; Gaps 1;

Qy 1 CDC---RGDCFC 9

Db 14 CDCGGERGECVC 25

RESULT 9

S29214
neurotoxin Tx2 - spider (Phoneutria nigriventer)

C;Species: Phoneutria nigriventer
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 07-May-1999
C;Accession: S29214
R;do Nascimento Cordeiro, M.; Ribeiro Diniz, C.; do Carmo Valentim, A.; von Eickstedt, V
FEBS Lett. 310, 153-156, 1992
A;Title: The purification and amino acid sequences of four Tx2 neurotoxins from the venom
A;Reference number: S29214; MUID:93011905; PMID:1397265
A;Accession: S29214
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-53 <COR>
C;Superfamily: curatatoxin

Query Match 65.4%; Score 42.5; DB 2; Length 53;
Best Local Similarity 58.3%; Pred. No. 7.7;
Matches 7; Conservative 1; Mismatches 1; Indels 3; Gaps 1;

Qy 1 CDC---RGDCFC 9

Db 14 CDCGGERGECVC 25

RESULT 9

A55011
metallothionein-like protein YOR031w - yeast (Saccharomyces cerevisiae)

C;Alternate names: protein O3675
C;Species: Saccharomyces cerevisiae
C;Date: 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change 19-Apr-2002
C;Accession: A55011; S66897
R;Culotta, V.C.; Howard, W.R.; Liu, X.F.
J. Biol. Chem. 269, 25295-25302, 1994
A;Title: CRS5 encodes a metallothionein-like protein in Saccharomyces cerevisiae.

Query Match 65.4%; Score 42.5; DB 2; Length 48;
Best Local Similarity 58.3%; Pred. No. 7.2;
Matches 7; Conservative 1; Mismatches 1; Indels 3; Gaps 1;

Qy 1 CDC---RGDCFC 9

Db 14 CDCGGERGECVC 25

```

A;Reference number: A55011; MUID:95014316; PMID:7929222
A;Accession: A55011
A;Molecule type: DNA
A;Residues: 1-69 <CU>
A;Cross-references: GB:L29056; NID:g499891; PIDN:AAA65061.1; PID:g499892
R;de Haan, M.; Grivell, L.A.; Maarse, A.C.
submitted to the Protein Sequence Database, July 1996
A;Reference number: S66877
A;Accession: S66897
A;Molecule type: DNA
A;Residues: 1-8 <DEH>
A;Cross-references: EMBL:Z74939; MTPS:YOR031w
A;Experimental source: strain S288C
A;Note: in strain S288C YOR031w is a pseudogene with an inframe stopcodon
C;Genetics:
A;Gene: SGD:CRS5; CRS5
A;Cross-references: SGD:S0005557
A;Map position: 15R
A;Note: YOR031w
C;Function:
A;Description: involved in copper homeostasis and detoxification

Query Match      63.1%; Score 41; DB 2; Length 69;
Best Local Similarity 71.4%; Pred. No. 15;
Matches      5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 CDCRGDC 7
      ||| | |
Db      6 CDCEGEC 12

RESULT 10
A84306
hypothetical protein Vng1524c [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C;Accession: A84306
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.;
Leichauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablon
Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
A;Title: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950
A;Accession: A84306
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-458 <STO>
A;Cross-references: GB:AE004437; NID:gi0581011; PIDN:AAG19813.1; GSPDB:GN00138
C;Genetics:
A;Gene: VNG1524C
C;Superfamily: ornithine-oxo-acid aminotransferase

Query Match      63.1%; Score 41; DB 2; Length 458;
Best Local Similarity 55.6%; Pred. No. 64;
Matches      5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy      1 CDCRGDCFC 9
      ||| | |
Db      198 CTCEGECSC 206

RESULT 11
T06757
hypothetical protein F15B8.180 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 22-Oct-1999
C;Accession: T06757
R;Quefrier, F.; Benes, V.; Rechmann, S.; Borkova, D.; Ansoorge, W.; Salanoubat, M.; Mewes,
submitted to the Protein Sequence Database, April 1999
A;Reference number: Z15794
A;Accession: T06757
A;Molecule type: DNA

A;Residues: 1-736 <QUE>
A;Cross-references: EMBL:AL049660; GSPDB:GN00061; ATSP:F15B8.180
A;Experimental source: cultivar Columbia; BAC clone F15B8
C;Genetics:
A;Gene: ATSP:F15B8.180
A;Map position: 3
A;Introns: 114/3; 146/1; 208/2; 293/3; 365/3; 384/3; 429/3; 467/3; 536/2; 563/2; 640/3

Query Match      63.1%; Score 41; DB 2; Length 736;
Best Local Similarity 53.8%; Pred. No. 91;
Matches      7; Conservative 1; Mismatches 1; Indels 4; Gaps 1;

Qy      1 CDCRGDC---FC 9
      ||| | |
Db      257 CDCKYDCLWGRCF 269

RESULT 12
T23433
hypothetical protein K08C7.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Jan-2000
C;Accession: T23433
R;Berks, M.
submitted to the EMBL Data Library, March 1996
A;Reference number: Z19740
A;Accession: T23433
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-3672 <WIL>
A;Cross-references: EMBL:Z70286; PIDN:CAA94293.1; GSPDB:GN00022; CESP:K08C7.3
A;Experimental source: clone K08C7
C;Genetics:
A;Gene: CESP:K08C7.3
A;Map position: 4
A;Introns: 66/1; 284/3; 563/1; 1187/3; 1248/3; 1300/1; 1460/1; 1623/3; 2361/3; 2988/3; 32
C;Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like h

Query Match      63.1%; Score 41; DB 2; Length 3672;
Best Local Similarity 55.6%; Pred. No. 38+02;
Matches      5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy      1 CDCRGDCFC 9
      ||| | |
Db      668 CDSNGQCYC 676

RESULT 13
T37316
Probable laminin alpha chain - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Jan-2000
C;Accession: T37316
R;Joh, K.; Zhu, K.; Hedgecock, E.M.; Inoue, T.; Hori, K.
submitted to the EMBL Data Library, August 1998
A;Description: Laminin alpha chain gene in the nematode C. elegans.
A;Reference number: Z21681
A;Accession: T37316
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-3704 <JOH>
A;Cross-references: EMBL:AB016806; PIDN:BA32347.1
A;Experimental source: strain N2
C;Genetics:
A;Gene: epi-1
A;Map position: IV
A;Introns: 66/1; 284/3; 563/1; 1187/3; 1248/3; 1300/1; 1460/1; 1623/3; 2361/3; 2988/3; 32
C;Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like h

Query Match      63.1%; Score 41; DB 2; Length 3704;
Best Local Similarity 55.6%; Pred. No. 38+02;
Matches      5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```

QY 1 CDCRGDCFC 9
Db 668 CDSNGQCFC 676

RESULT 14
TVVPA
small T antigen - mouse polyomavirus
C:Species: Polyomavirus muris (mouse polyomavirus)
C:Date: 31-Jul-1980 #sequence_revision 31-Jul-1980 #text_change 24-Sep-1999
C:Accession: C03635; B36761; A03614
R:Soeda, E.; Arrand, J.R.; Smolar, N.; Walsh, J.E.; Griffin, B.E.
Nature 283, 445-453, 1980
A:Title: Coding potential and regulatory signals of the polyoma virus genome.
A:Reference number: A03635; MUID:80099647; PMID:6243401
A:Accession: C03635
A:Molecule type: DNA
A:Residues: 1-195 <SOE>
A:Cross-references: GB:J02288; GB:J02290; GB:J02291; GB:J02292; GB:K00932; GB:K00997; GB:K00998
A:Experimental source: strain A2
R:Friedmann, T.; Esty, A.; LaPorte, P.; Deininger, P.
Cell 17, 715-724, 1979
A:Title: The nucleotide sequence and genome organization of the polyoma early region: ex
A:Reference number: A36761; MUID:80001963; PMID:225042
A:Accession: B36761
A:Molecule type: DNA
A:Residues: 1-195 <FRI>
A:Cross-references: GB:J02288; GB:J02290; GB:J02291; GB:J02292; GB:K00932; GB:K00997; GB:K00998
A:Experimental source: strain 3
R:Rothwell, V.M.; Polk, W.R.
J. Virol. 48, 472-480, 1983
A:Title: Comparison of the DNA sequence of the Crawford small-plaque variant of polyomav
A:Reference number: A28838; MUID:84011043; PMID:6312103
A:Accession: C28838
A:Molecule type: DNA
A:Residues: 1-195 <ROT>
A:Cross-references: GB:K02737; MUID:5332788
A:Experimental source: strain Crawford small-plaque
C:Keywords: early protein
C:Genetics:
A:Introns: 192/1
A:Superfamily: small T antigen; dnaJ amino-terminal homology
C:Keywords: early protein
F:12-62/Domain: dnaJ amino-terminal homology #status atypical <DNJ>

Query Match 61.5%; Score 40; DB 1; Length 195;
Best Local Similarity 53.8%; Pred. No. 47;
Matches 7; Conservative 1; Mismatches 1; Indels 4; Gaps 1;

QY 1 CDCR----GDCFC 9
Db 138 CDARCLVLGECFC 150

RESULT 15
S22562
small T antigen - mouse plasmid L factor
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 26-Aug-1999
C:Accession: S22562
R:Yoshimura, H.; Ikeda, Y.; Yoshimoto, M.; Tamaki, S.; Hanada, K.; Kusano, T.; Kohda, T.
Nucleic Acids Res. 19, 3633-3639, 1991
A:Title: Structural and functional analysis of a polyoma-related mammalian plasmid (L fa
A:Reference number: S22560; MUID:91305109; PMID:1649455
A:Accession: S22562
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-195 <YOS>
A:Cross-references: EMBL:X59849; NID:952899; PIDN:CAA42512.1; PID:952902
C:Genetics:
A:Genome: Plasmid
A:Introns: 192/1
C:Superfamily: small T antigen; dnaJ amino-terminal homology

F:12-62/Domain: dnaJ amino-terminal homology #status atypical <DNJ>

Query Match 61.5%; Score 40; DB 2; Length 195;
Best Local Similarity 53.8%; Pred. No. 47;
Matches 7; Conservative 1; Mismatches 1; Indels 4; Gaps 1;

QY 1 CDCR----GDCFC 9

Db 138 CDARCLVLGECFC 150

Search completed: July 11, 2004, 09:17:02
Job time : 22 secs

GenCore-version 5.1.6
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OM protein - protein search, using sw model

Run on: July 11, 2004, 09:14:02 ; Search time 11 Seconds
(without alignments)
42.603 Million cell updates/sec

Title: US-09-734-628-1
Perfect score: 65
Sequence: 1 CDCRGDFC 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	44	67.7	577	1TB6_CAVPO	P18583 cavia porce
2	44	67.7	787	1TB6_MOUSE	Q92059 mus musculus
3	44	67.7	788	1TB6_HUMAN	P18564 homo sapien
4	43	66.2	1627	1PAPA_HUMAN	Q13219 homo sapien
5	43	66.2	4753	1LRP_CABEL	Q04833 caenorhabdi
6	42.5	65.4	49	1TX25_PHONI	P29424 phoneutria
7	42.5	65.4	82	1TX26_PHONI	P29425 phoneutria
8	42.5	65.4	82	1TXSA_PHONI	O76199 phoneutria
9	42.5	65.4	88	1TX21_PHONI	P29423 phoneutria
10	42.5	65.4	115	1TX1A_PHONI	O76198 phoneutria
11	41	63.1	69	1CRS5_YEAST	P41902 saccharomyc
12	41	63.1	3672	1LML2_CABEL	Q21313 caenorhabdi
13	40.5	62.3	799	1ITBN_DROME	Q27591 drosophila
14	40	61.5	195	1TASM_POVMA	P03078 mouse polyo
15	40	61.5	421	1TAMI_POVMA	P03077 mouse polyo
16	40	61.5	421	1TAMI_POVMC	P12906 mouse polyo
17	40	61.5	440	1TAMI_POVW3	P03076 mouse polyo
18	39.5	60.8	246	1AEG_RAT	P12020 rattus norv
19	39.5	60.8	423	1TIC2_MOUSE	Q9er58 mus musculu
20	39	60.0	30	1ITR1_MONCH	P10294 momordica c
21	39	60.0	30	1ITR3_MONCH	P82410 momordica c
22	39	60.0	60	1MTA_CHAAC	P52724 chaenoceph
23	39	60.0	60	1MTA_CHIHA	Q13258 chionodraco
24	39	60.0	60	1MTA_NOTCO	O73914 notothenia
25	39	60.0	60	1MTA_PAGBE	Q93609 pagothenia
26	39	60.0	60	1MTA_SPAAU	P52727 sparua
27	39	60.0	60	1MTB_CHAAC	P52724 chaenoceph
28	39	60.0	60	1MTB_CHIHA	Q13259 chionodraco
29	39	60.0	60	1MTB_DICLA	Q9pt99 dicentrarch
30	39	60.0	60	1MTB_PAGBE	P52726 oreochromis
31	39	60.0	60	1MT_OREMO	P52726 oreochromis
32	39	60.0	60	1MT_PAGMA	Q9ib50 pagrus majo
33	39	60.0	60	1MT_PARCR	O93450 parachaenic

ALIGNMENTS

```

RESULT 1
1TB6_CAVPO
ID 1TB6_CAVPO STANDARD; PRT; 577 AA.
AC P18563;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Integrin beta-6 (Fragment).
GN ITGB6
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Hartley;
RX MEDLINE=90307659; PubMed=2365683;
RA Sheppard D., Rozzo C., Starr L., Quaranta V., Erle D.J., Pytela R.;
RT "Complete amino acid sequence of a novel integrin beta subunit (beta
RT 6) identified in epithelial cells using the polymerase chain
RT reaction."
RL J. Biol. Chem. 265:11502-11507(1990).
CC -!- FUNCTION: INTEGRIN ALPHA-V/BETA-6 IS A RECEPTOR FOR FIBRONECTIN
CC AND CYTOTACTIN. IT RECOGNIZES THE SEQUENCE R-G-D IT ITS LIGANDS.
CC -!- SUBUNIT: Heterodimer of an alpha and a beta subunit. Beta-6
CC associates with alpha-V. Interacts with FLNB (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Belongs to the integrin beta chain family.
CC -!- SIMILARITY: Contains 2 WFA-like domains.
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CC -----
CC EMBL; M35197; AAA37043.1; -
CC EMBL; A26611; AAA01833.1; -
CC PIR; B37057; B37057.
CC HSSP; P05106; 1JUV2.
CC InterPro: IPR006209; EGF like.
CC InterPro: IPR002369; Integrin_B.
CC InterPro: IPR001169; Integrin_Beta_C.
CC Pfam; PF00362; Integrin_B; 1.
CC PRINTS; PR01186; INTEGRINB.
CC ProDom; PD001811; Integrin_B; 1.
CC SMART; SM00187; INB; 1.
CC PROSITE; PS00243; INTEGRIN_BETA; 2.
CC PROSITE; PS00022; EGF_1; UNKNOWN_2.
CC PROSITE; PS01186; EGF_2; UNKNOWN_1.
CC Integrin; Cell adhesion; Receptor; Transmembrane; Glycoprotein;
CC Repeat.
CC NON_TER 1
CC DOMAIN <1 566 EXTRACELLULAR (POTENTIAL).

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34 39 60.0 60 1 MT_PRRFL PS2725 perca fluvi
35 39 60.0 60 1 MT_PLEPL P07216 pleuronecte
36 39 60.0 60 1 MT_PSEAM P55945 pseudopleur
37 39 60.0 61 1 MTIA_BOVIN P04356 bos taurus
38 39 60.0 61 1 MTIA_PIG P49068 sus scrofa
39 39 60.0 61 1 MTIB_SHEEP P09577 ovis aries
40 39 60.0 61 1 MTIC_PIG P79376 sus scrofa
41 39 60.0 61 1 MTIS_SHEEP P09578 ovis aries
42 39 60.0 61 1 MTIE_PIG P79431 sus scrofa
43 39 60.0 65 1 MT_PARLI P80367 paracentrot
44 39 60.0 68 1 MT3_HORSE P37360 equus cabal
45 39 60.0 624 1 SUV4_ARATH Q8gzb6 arabidopsis

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FT CARBOHYD 260 260 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 387 387 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 396 396 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 471 471 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 541 541 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 575 575 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 788 AA; 85935 MW; EDB7D533EC4C8C4D CRC64;

Query Match 67.7%; Score 44; DB 1; Length 788;
 Best Local Similarity 66.7%; Pred. No. 10;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CDCRGDCFC 9
 Db 511 CSGRGDCVC 519

RESULT 4
 PAPA HUMAN STANDARD; PRT; 1627 AA.
 AC Q13219; Q08371; Q9UDK7;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Papalysin-1 precursor (EC 3.4.24.79) (Pregnancy-associated plasma
 DE protein-A) (PAPP-A) (Insulin-like growth factor-dependent IGF binding
 DE protein-4 protease) (IGF-dependent IGFBP-4 protease) (IGFBP-4ase).
 GN PAPP-A.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 [1]
 RP SEQUENCE FROM N.A., AND INDUCTION.
 RC TISSUE=Placenta;
 RX MEDLINE=96203921; PubMed=8620868;
 RA Haaning J., Oxvig C., Overgaard M.T., Ebbesen P., Kristensen T.,
 RA Sottrup-Jensen L.;
 RT "Complete cDNA sequence of the preproform of human pregnancy-
 RT associated plasma protein-A. Evidence for expression in the brain and
 RT induction by CAMP.";
 RL Eur. J. Biochem. 237:159-163(1996).
 [2]
 RP SEQUENCE OF 77-1627 FROM N.A. SEQUENCE OF 81-98; 117-126; 210-224;
 RP 468-485; 507-519; 576-593; 609-621; 718-736; 742-754; 1006-1017;
 RP 1259-1273; 1369-1374; 1389-1398; 1490-1509; 1524-1533 AND 1537-1544,
 RP VARIANT SER-944, AND TISSUE SPECIFICITY.
 RC TISSUE=Placenta, and Serum;
 RX MEDLINE=94146014; PubMed=7508748;
 RA Kristensen T., Oxvig C., Sand O., Møller N.P.H., Sottrup-Jensen L.;
 RA "Amino acid sequence of human pregnancy-associated plasma protein-A
 RT derived from cloned cDNA.";
 RT Biochemistry 33:1592-1598(1994).
 [3]
 RP SEQUENCE OF 81-89; 117-126; 210-224; 460-485; 507-519; 576-593;
 RP 718-736; 742-754; 1259-1273; 1369-1374; 1490-1509; 1524-1533 AND
 RP 1537-1544, SUBUNITS, AND INTERCHAIN DISULFIDE BOND.
 RC TISSUE=Serum;
 RX MEDLINE=93286045; PubMed=7685339;
 RA Oxvig C., Sand O., Kristensen T., Gleich G.J., Sottrup-Jensen L.;
 RA "Circulating human pregnancy-associated plasma protein-A is disulfide-
 RT bridged to the proform of eosinophil major basic protein.";
 RT J. Biol. Chem. 268:12243-12246(1993).
 [4]
 RP PARTIAL SEQUENCE, CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS.
 RX MEDLINE=22421368; PubMed=12421832;
 RA Overgaard M.T., Sørensen E.S., Stachowiak D., Boldt H.B.,
 RA Kristensen L., Sottrup-Jensen L., Oxvig C.;
 RT "Complex of pregnancy-associated plasma protein-A and the proform of
 RT eosinophil major basic protein. Disulfide structure and carbohydrate
 RT attachment sites.";
 RT J. Biol. Chem. 278:2106-2117(2003).
 [5]
 RN IDENTIFICATION, FUNCTION, SUBCELLULAR LOCATION, AND TISSUE
 RP SPECIFICITY.
 RC TISSUE=Fibroblast;
 RX MEDLINE=99179030; PubMed=10077652;
 RA Lawrence J.B., Oxvig C., Overgaard M.T., Sottrup-Jensen L.,
 RA Gleich G.J., Hays L.G., Yates J.R. III, Conover C.A.;
 RT "The insulin-like growth factor (IGF)-dependent protein-4
 RT protease secreted by human fibroblasts is pregnancy-associated plasma
 RT protein-A.";
 RL Proc. Natl. Acad. Sci. U.S.A. 96:3149-3153(1999).
 [6]
 RN FUNCTION, SUBUNITS, AND ENZYME REGULATION.
 RP MEDLINE=20469470; PubMed=10913121;
 RX Overgaard M.T., Haaning J., Boldt H.B., Olsen I.M., Laursen L.S.,
 RA Christiansen M., Gleich G.J., Sottrup-Jensen L., Conover C.A.,
 RA Oxvig C.;
 RT "Expression of recombinant human pregnancy-associated plasma protein-A
 RT and identification of the proform of eosinophil major basic protein
 RT as its physiological inhibitor.";
 RL J. Biol. Chem. 275:31128-31133(2000).
 [7]
 RN TISSUE SPECIFICITY.
 RP MEDLINE=95057018; PubMed=7526035;
 RX Bonno M., Oxvig C., Kephart G.M., Wagner J.M., Kristensen T.,
 RA Sottrup-Jensen L., Gleich G.J.;
 RT "Localization of pregnancy-associated plasma protein-A and
 RT colocalization of pregnancy-associated plasma protein-A messenger
 RT ribonucleic acid and eosinophil granule major basic protein messenger
 RT ribonucleic acid in placenta.";
 RL Lab. Invest. 71:560-566(1994).
 [8]
 RN TISSUE SPECIFICITY, AND DEVELOPMENTAL STAGE.
 RP MEDLINE=99423540; PubMed=10491647;
 RX Overgaard M.T., Oxvig C., Christiansen M., Lawrence J.B.,
 RA Conover C.A., Gleich G.J., Sottrup-Jensen L., Haaning J.;
 RT "Messenger ribonucleic acid levels of pregnancy-associated plasma
 RT protein-A and the proform of eosinophil major basic protein:
 RT expression in human reproductive and nonreproductive tissues.";
 RL Biol. Reprod. 61:1083-1089(1999).
 [9]
 RN DEVELOPMENTAL STAGE.
 RP MEDLINE=95293954; PubMed=7539791;
 RX Oxvig C., Haaning J., Kristensen L., Wagner J.M., Rubin I.,
 RA Stibrand T., Gleich G.J., Sottrup-Jensen L.;
 RT "Identification of angiotensinogen and complement C3dg as novel
 RT proteins binding the proform of eosinophil major basic protein in
 RT human pregnancy serum and plasma.";
 RL J. Biol. Chem. 270:13645-13651(1995).
 CC -!- FUNCTION: Metalloproteinase which specifically cleaves IGFBP-4 in
 CC the presence of IGF, resulting in release of bound IGF.
 CC -!- CATALYTIC ACTIVITY: Cleavage of the 135-Met-Lys-136 bond in
 CC insulin-like growth factor binding protein (IGFBP)-4, and the 143-
 CC Ser-Lys-144 bond in IGFBP-5.
 CC -!- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
 CC -!- ENZYME REGULATION: Inhibited by complexation with the proform
 CC of PRG2.
 CC -!- SUBUNIT: Homodimer; disulfide-linked. In pregnancy serum,
 CC predominantly found as a disulfide-linked 2:2 heterotetramer with
 CC the proform of PRG2.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: High levels in placenta and pregnancy serum.
 CC In placenta, expressed in X cells in septa and anchoring villi,
 CC and in syncytiotrophoblasts in the chorionic villi. Lower levels
 CC are found in a variety of other tissues including kidney,
 CC myometrium, endometrium, ovaries, breast, prostate, bone marrow,
 CC colon, fibroblasts and osteoblasts.
 CC -!- DEVELOPMENTAL STAGE: Present in serum and placenta during
 CC pregnancy; levels increase throughout pregnancy.
 CC -!- INDUCTION: By 8-bromoadenosine-3',5'-phosphate.
 CC -!- PTM: There appear to be no free sulfhydryl groups.
 CC -!- SIMILARITY: Contains 5 Sushi (SCR) domains.
 CC -!- SIMILARITY: Belongs to peptidase family M43B.

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CC -----
DR EMBL; U28727; AAC50543.1; -;
DR EMBL; X68280; CAA48341.1; -;
DR PIR; S65464; S65464.
DR MEROPS; M43.004; -;
DR Genew; HGNC:8602; PAPP. A.
DR MIM; 176385; -;
DR GO; GO:0005576; Cxetracellular; IDA.
DR GO; GO:0008237; Fmetallopeptidase activity; IDA.
DR GO; GO:0008270; Fzinc ion binding; NAS.
DR GO; GO:0007565; P:pregnancy; NAS.
DR InterPro; IPR008985; ConA like lec_g1.
DR InterPro; IPR006558; LamG like dom.
DR InterPro; IPR000800; Notch dom.
DR InterPro; IPR008025; Pept_M_Zn_BS.
DR InterPro; IPR008754; Peptidase M43B.
DR InterPro; IPR000436; Sushi_SCR_CCP.
DR Pfam; PF05572; Peptidase M46; 1.
DR Pfam; PF00084; sushi; 4.
DR SMART; SM00032; CCP; 4.
DR SMART; SM00560; LamGL; 1.
DR SMART; SM00004; NL; 3.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
KW Hydroxylase; Metalloprotease; Metal-binding; Zinc; Signal; Glycoprotein;
KW Zymogen; Repeat; Sushi.
FT SIGNAL 1 22 POTENTIAL.
FT PROPEP 23 80
FT CHAIN 81 1627 PAPALYSIN-1.
FT DOMAIN 24 83 ARG-RICH.
FT DOMAIN 272 583 PROTEOLYTIC.
FT DOMAIN 1215 1280 SUSHI 1.
FT DOMAIN 1285 1342 SUSHI 2.
FT DOMAIN 1346 1410 SUSHI 3.
FT DOMAIN 1415 1471 SUSHI 4.
FT DOMAIN 1478 1554 SUSHI 5.
FT METAL 562 562 ZINC (CATALYTIC) (BY SIMILARITY).
FT ACT_SITE 563 563 BY SIMILARITY.
FT METAL 566 566 ZINC (CATALYTIC) (BY SIMILARITY).
FT DISULFID 144 235
FT DISULFID 327 622
FT DISULFID 332 657
FT DISULFID 414 428
FT DISULFID 424 440
FT DISULFID 457 473
FT DISULFID 461 461
FT DISULFID 474 485
FT DISULFID 583 600
FT DISULFID 587 612
FT DISULFID 710 878
FT DISULFID 713 881
FT DISULFID 732 732
FT DISULFID 753 835
FT DISULFID 775 781
FT DISULFID 947 975
FT DISULFID 960 971
FT DISULFID 983 990
FT DISULFID 999 1011
FT DISULFID 1036 1070
FT DISULFID 1051 1139
FT DISULFID 1192 1205
FT DISULFID 1210 1210
FT DISULFID 1215 1269
FT DISULFID 1227 1238
FT DISULFID 1242 1285
FT DISULFID 1285 1329

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EMBL; U28727; AAC50543.1; -;
EMBL; X68280; CAA48341.1; -;
PIR; S65464; S65464.
MEROPS; M43.004; -;
Genew; HGNC:8602; PAPP. A.
MIM; 176385; -;
GO; GO:0005576; Cxetracellular; IDA.
GO; GO:0008237; Fmetallopeptidase activity; IDA.
GO; GO:0008270; Fzinc ion binding; NAS.
GO; GO:0007565; P:pregnancy; NAS.
InterPro; IPR008985; ConA like lec_g1.
InterPro; IPR006558; LamG like dom.
InterPro; IPR000800; Notch dom.
InterPro; IPR008025; Pept_M_Zn_BS.
InterPro; IPR008754; Peptidase M43B.
InterPro; IPR000436; Sushi_SCR_CCP.
Pfam; PF05572; Peptidase M46; 1.
Pfam; PF00084; sushi; 4.
SMART; SM00032; CCP; 4.
SMART; SM00560; LamGL; 1.
SMART; SM00004; NL; 3.
PROSITE; PS00142; ZINC_PROTEASE; 1.
Hydroxylase; Metalloprotease; Metal-binding; Zinc; Signal; Glycoprotein;
Zymogen; Repeat; Sushi.
SIGNAL 1 22 POTENTIAL.
PROPEP 23 80
CHAIN 81 1627 PAPALYSIN-1.
DOMAIN 24 83 ARG-RICH.
DOMAIN 272 583 PROTEOLYTIC.
DOMAIN 1215 1280 SUSHI 1.
DOMAIN 1285 1342 SUSHI 2.
DOMAIN 1346 1410 SUSHI 3.
DOMAIN 1415 1471 SUSHI 4.
DOMAIN 1478 1554 SUSHI 5.
METAL 562 562 ZINC (CATALYTIC) (BY SIMILARITY).
ACT_SITE 563 563 BY SIMILARITY.
METAL 566 566 ZINC (CATALYTIC) (BY SIMILARITY).
DISULFID 144 235
DISULFID 327 622
DISULFID 332 657
DISULFID 414 428
DISULFID 424 440
DISULFID 457 473
DISULFID 461 461
DISULFID 474 485
DISULFID 583 600
DISULFID 587 612
DISULFID 710 878
DISULFID 713 881
DISULFID 732 732
DISULFID 753 835
DISULFID 775 781
DISULFID 947 975
DISULFID 960 971
DISULFID 983 990
DISULFID 999 1011
DISULFID 1036 1070
DISULFID 1051 1139
DISULFID 1192 1205
DISULFID 1210 1210
DISULFID 1215 1269
DISULFID 1227 1238
DISULFID 1242 1285
DISULFID 1285 1329

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EMBL; M96150; AAA28105.1; -;
EMBL; Z73907; CAA98124.1; -;
PIR; A47437; A47437.
HSP; O07954; 1CR8.
WormPep; P29D11.1; CE05765.
InterPro; IPR000152; Asx_hydroxyl_S.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR006209; EGF_like.
InterPro; IPR002172; LDL_receptor_A.
InterPro; IPR000033; Ldl_receptor_rep.
Pfam; PF00057; ldl_recept_a; 34.
Pfam; PF00058; ldl_recept_b; 26.
PRINTS; PR00261; LDLRECEPTOR.
SMART; SM00179; EGF_CA; 2.
SMART; SM00192; LDLA; 35.
SMART; SM00135; LY; 32.
PROSITE; PS00010; ASX_HYDROXYL; 6.
PROSITE; PS00022; EGF_1; 1.
PROSITE; PS01186; EGF_2; 3.
PROSITE; PS00026; EGF_3; 2.
PROSITE; PS01187; EGF_CA; 3.
PROSITE; PS01209; LDLRA_1; 27.

FT DISULFID 1300 1310
Query Match 66.2%; Score 43; DB 1; Length 1627;
Best Local Similarity 66.7%; Pred. No. 28;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 CDCRGDCFC 9
DB 1600 CDLQGDCA 1608
RESULT 5
LRP CAEL STANDARD; PRT; 4753 AA.
AC Q04833;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Low-density lipoprotein receptor-related protein precursor (LRP).
GN LRP-1 OR F29D11.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93281621; PubMed=8506301;
RA Yochem J., Greenwald I.;
RT "A gene for a low density lipoprotein receptor-related protein in the
RL nematode Caenorhabditis elegans.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:4572-4576 (1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Wilkinson J.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: May act as a receptor for the endocytosis of
CC extracellular ligands such as chylomicron remnants, protease-
CC inhibitor complexes and vitellogenin.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Contains 35 LDL-receptor class A domains.
CC -!- SIMILARITY: Contains 17 EGF-like domains.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
EMBL; M96150; AAA28105.1; -;
EMBL; Z73907; CAA98124.1; -;
PIR; A47437; A47437.
HSP; O07954; 1CR8.
WormPep; P29D11.1; CE05765.
InterPro; IPR000152; Asx_hydroxyl_S.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR006209; EGF_like.
InterPro; IPR002172; LDL_receptor_A.
InterPro; IPR000033; Ldl_receptor_rep.
Pfam; PF00057; ldl_recept_a; 34.
Pfam; PF00058; ldl_recept_b; 26.
PRINTS; PR00261; LDLRECEPTOR.
SMART; SM00179; EGF_CA; 2.
SMART; SM00192; LDLA; 35.
SMART; SM00135; LY; 32.
PROSITE; PS00010; ASX_HYDROXYL; 6.
PROSITE; PS00022; EGF_1; 1.
PROSITE; PS01186; EGF_2; 3.
PROSITE; PS00026; EGF_3; 2.
PROSITE; PS01187; EGF_CA; 3.
PROSITE; PS01209; LDLRA_1; 27.

Db 361 CSCI GDCF 368

RESULT 6

TX25_PHONI

ID TX25_PHONI STANDARD; PRT; 49 AA.

AC P29424;

DT 01-APR-1993 (Rel. 25, Created)

DT 01-APR-1993 (Rel. 25, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Neurotoxin Tx2-5

OS Phoneutria nigriventer (Brazilian armed spider).

OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;

OC Araneomorphae; Entelegynae; Lycosoidea; Ctenidae; Phoneutria.

OX NCBI_TaxID=6918;

RN [1]

RP SEQUENCE

RC TISSUE=Venom; PubMed=1397265;

RX MEDLINE=92011905; Valentim A.D.C., von Eickstedt V.R.D.,

RA Cordeiro M.N., Diniz C.R., Valentim A.D.C., von Eickstedt V.R.D.,

RA Gilroy J., Richardson M.;

RT "The purification and amino acid sequences of four Tx2 neurotoxins

RT from the venom of the Brazilian 'armed' spider Phoneutria nigriventer

RT (Keys).";

RL FEBS Lett. 310:153-156(1992).

RN [2]

RP SEQUENCE OF 1-10.

RC TISSUE=Venom;

RX MEDLINE=92196803; PubMed=1801316;

RX Rezende L. Jr., Cordeiro M.N., Oliveira E.B., Diniz C.R.;

RT "Isolation of neurotoxic peptides from the venom of the 'armed'

RT spider Phoneutria nigriventer.;"

RL Toxicon 29:1225-1233(1991).

CC -1- FUNCTION: Blocks voltage-gated sodium channels. Causes scratching,

CC lacticrimation, hypersalivation, sweating and agitation followed by

CC spastic paralysis of the anterior and posterior extremities and

CC death at dose levels of 0.24 mg/mouse. Insecticidal to the larval

CC and adult forms of the house fly.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.

CC -1- SIMILARITY: Belongs to the spider toxin Tx2 family.

DR PIR; S29215; S29215.

KW Sodium channel inhibitor; Toxin; Neurotoxin; Ionic channel inhibitor;

SQ SEQUENCE 49 AA; 5111 MW; 77B46AAB3911716 CRC64;

Query Match 65.4%; Score 42.5; DB 1; Length 49;

Best Local Similarity 58.3%; Pred. No. 1.3;

Matches 7; Conservative 1; Mismatches 1; Indels 3; Gaps 1;

QY 1 CDC---RGDCFC 9

Db 14 CDCGGERGECVC 25

RESULT 7

TX26_PHONI

ID TX26_PHONI STANDARD; PRT; 82 AA.

AC P29425; Q95UF2;

DT 01-APR-1993 (Rel. 25, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Neurotoxin Tx2-6 precursor.

OS Phoneutria nigriventer (Brazilian armed spider).

OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;

OC Araneomorphae; Entelegynae; Lycosoidea; Ctenidae; Phoneutria.

OX NCBI_TaxID=6918;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Venom gland;

RX MEDLINE=99053403; PubMed=9839668;

RA Kalapothakis E., Penaforte C.L., Beirao P.S.L., Romano-Silva M.A.,

RA Cruz J.S., Prado M.A.M., Guimaraes P.E.M., Gomez M.V., Prado V.F.;

RT "Cloning of cDNAs encoding neurotoxic peptides from the spider

RT Phoneutria nigriventer.;"

RL Toxicon 36:1843-1850(1998).

CC -1- FUNCTION: Blocks voltage-gated sodium channels (By similarity).

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.

CC -1- SIMILARITY: Belongs to the spider toxin Tx2 family.

Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.

[2]

SEQUENCE OF 35-82 FROM N.A.

TISSUE=Venom;

MEDLINE=93011905; PubMed=1397265;

Cordeiro M.N., Diniz C.R., Valentim A.D.C., von Eickstedt V.R.D.,

Gilroy J., Richardson M.;

"The purification and amino acid sequences of four Tx2 neurotoxins

from the venom of the Brazilian 'armed' spider Phoneutria nigriventer

(Keys).";

FEBS Lett. 310:153-156(1992).

-1- FUNCTION: Blocks voltage-gated sodium channels. Causes scratching,

lacticrimation, hypersalivation, sweating and agitation followed by

spastic paralysis of the anterior and posterior extremities and

death at dose levels of 0.79 mg/mouse. It significantly activates

voltage-dependent sodium channels. Insecticidal to the larval and

adult forms of the house fly.

-1- SUBCELLULAR LOCATION: Secreted.

-1- TISSUE SPECIFICITY: Expressed by the venom gland.

-1- SIMILARITY: Belongs to the spider toxin Tx2 family.

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EMBL; AY054746; AAL14349.1; -

PIR; S29216; S29216.

Sodium channel inhibitor; Toxin; Neurotoxin; Ionic channel inhibitor;

Signal.

SIGNAL 1 17 POTENTIAL.

PROPEP 18 34

CHAIN 35 81 NEUROTOXIN TX2-6.

PROPEP 82 82

SEQUENCE 82 AA; 9031 MW; F4CEA5E7B8D53E59 CRC64;

Query Match 65.4%; Score 42.5; DB 1; Length 82;

Best Local Similarity 58.3%; Pred. No. 2;

Matches 7; Conservative 1; Mismatches 1; Indels 3; Gaps 1;

QY 1 CDC---RGDCFC 9

Db 48 CDCGGERGECVC 59

RESULT 8

TX5A_PHONI

ID TX5A_PHONI STANDARD; PRT; 82 AA.

AC O76199;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Neurotoxin Pn2-5A precursor.

OS Phoneutria nigriventer (Brazilian armed spider).

OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;

OC Araneomorphae; Entelegynae; Lycosoidea; Ctenidae; Phoneutria.

OX NCBI_TaxID=6918;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Venom gland;

RX MEDLINE=99053403; PubMed=9839668;

RA Kalapothakis E., Penaforte C.L., Beirao P.S.L., Romano-Silva M.A.,

RA Cruz J.S., Prado M.A.M., Guimaraes P.E.M., Gomez M.V., Prado V.F.;

RT "Cloning of cDNAs encoding neurotoxic peptides from the spider

RT Phoneutria nigriventer.;"

RL Toxicon 36:1843-1850(1998).

CC -1- FUNCTION: Blocks voltage-gated sodium channels (By similarity).

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.

CC -1- SIMILARITY: Belongs to the spider toxin Tx2 family.

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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF014463; AAC26165.1; -.
KW Sodium channel inhibitor; Toxin; Neurotoxin; Ionic channel inhibitor;
KW Signal.
FT SIGNAL. 1 17 POTENTIAL.
FT PROPEP 18 34 BY SIMILARITY.
FT CHAIN 35 81 NEUROTOXIN PN2-5A.
FT PROPEP 82 82 BY SIMILARITY.
FT PROPEP 82 82 BY SIMILARITY.
SQ SEQUENCE 82 AA; 8856 MW; 11DAF1EBE78B318F CRC64;

Query Match 65.4%; Score 42.5; DB 1; Length 82;
Best Local Similarity 58.3%; Pred. No. 2;
Matches 7; Conservative 1; Mismatches 1; Indels 3; Gaps 1;

QY 1 CDC---RGDCFC 9
DB 48 CDCCGERGECVC 59

RESULT 9
TX21_PHONI
ID TX21 PHONI STANDARD; PRT; 88 AA.
AC P29423;
DT 01-APR-1993 (Rel. 25, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Neurotoxin Tx2-1 precursor.
OS Phoneutria nigriventer (Brazilian armed spider).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
OC Araneomorphae; Entelegynae; Lycosoidea; Ctenidae; Phoneutria.
OX NCBI_TaxID=6918;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RX MEDLINE=99053403; PubMed=9839668;
RA Kalapothakis E., Penaforte C.L., Beirao P.S.L., Romano-Silva M.A.,
RA Cruz J.S., Prado M.A.M., Guimaraes P.E.M., Gomez M.V., Prado V.F.;
RA "Cloning of cDNAs encoding neurotoxic peptides from the spider
RT Phoneutria nigriventer.";
RT Toxicon 36:1843-1850(1998).
RN [2]
RP SEQUENCE OF 35-87.
RC TISSUE=Venom;
RX MEDLINE=93011905; PubMed=1397265;
RA Cordeliro M.N., Diniz C.R., Valentim A.D.C., von Eickstedt V.R.D.,
RA Gilroy J., Richardson M.;
RT "The purification and amino acid sequences of four Tx2 neurotoxins
RT from the venom of the Brazilian 'armed' spider Phoneutria nigriventer
RT (Keys).";
RL FEBS Lett. 310:153-156(1992).
CC -!- FUNCTION: Blocks voltage-gated sodium channels. Causes scratching,
CC lacrimation, hypersalivation, sweating and agitation followed by
CC spastic paralysis of the anterior and posterior extremities and
CC death at dose levels of 1.62 mg/mouse. Insecticidal to the larval
CC and adult forms of the house fly.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -!- SIMILARITY: Belongs to the spider toxin Tx2 family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF014464; AAC26166.1; -.
KW Sodium channel inhibitor; Toxin; Neurotoxin; Ionic channel inhibitor;
KW Signal.
FT SIGNAL. 1 17 POTENTIAL.
FT PROPEP 18 34 BY SIMILARITY.
FT CHAIN 35 81 NEUROTOXIN PN2-1A.
FT PROPEP 82 82 BY SIMILARITY.
FT PROPEP 88 88 BY SIMILARITY.
SQ SEQUENCE 88 AA; 9841 MW; D8AD07C6A769E647 CRC64;

Query Match 65.4%; Score 42.5; DB 1; Length 88;
Best Local Similarity 58.3%; Pred. No. 2;
Matches 7; Conservative 1; Mismatches 1; Indels 3; Gaps 1;

QY 1 CDC---RGDCFC 9
DB 48 CDCCGERGECVC 59

RESULT 10
TX1A_PHONI
ID TX1A PHONI STANDARD; PRT; 115 AA.
AC O76198;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neurotoxin Pn2-1A precursor.
OS Phoneutria nigriventer (Brazilian armed spider).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
OC Araneomorphae; Entelegynae; Lycosoidea; Ctenidae; Phoneutria.
OX NCBI_TaxID=6918;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RX MEDLINE=99053403; PubMed=9839668;
RA Kalapothakis E., Penaforte C.L., Beirao P.S.L., Romano-Silva M.A.,
RA Cruz J.S., Prado M.A.M., Guimaraes P.E.M., Gomez M.V., Prado V.F.;
RA "Cloning of cDNAs encoding neurotoxic peptides from the spider
RT Phoneutria nigriventer.";
RT Toxicon 36:1843-1850(1998).
RN [2]
RP SEQUENCE OF 35-87.
RC TISSUE=Venom;
RX MEDLINE=93011905; PubMed=1397265;
RA Cordeliro M.N., Diniz C.R., Valentim A.D.C., von Eickstedt V.R.D.,
RA Gilroy J., Richardson M.;
RT "The purification and amino acid sequences of four Tx2 neurotoxins
RT from the venom of the Brazilian 'armed' spider Phoneutria nigriventer
RT (Keys).";
RL FEBS Lett. 310:153-156(1992).
CC -!- FUNCTION: Blocks voltage-gated sodium channels. Causes scratching,
CC lacrimation, hypersalivation, sweating and agitation followed by
CC spastic paralysis of the anterior and posterior extremities and
CC death at dose levels of 1.62 mg/mouse. Insecticidal to the larval
CC and adult forms of the house fly.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -!- SIMILARITY: Belongs to the spider toxin Tx2 family.
CC -----
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CC -----
DR EMBL; AF014462; AAC26164.1; -.
KW Sodium channel inhibitor; Toxin; Neurotoxin; Ionic channel inhibitor;
KW Signal.
FT SIGNAL. 1 17 POTENTIAL.
FT PROPEP 18 61 BY SIMILARITY.
FT CHAIN 62 114 NEUROTOXIN PN2-1A.
FT PROPEP 115 115 BY SIMILARITY.
FT PROPEP 115 115 BY SIMILARITY.
SQ SEQUENCE 115 AA; 12858 MW; B7D321750F7BA50 CRC64;

Query Match 65.4%; Score 42.5; DB 1; Length 115;
Best Local Similarity 58.3%; Pred. No. 2;
Matches 7; Conservative 1; Mismatches 1; Indels 3; Gaps 1;

QY 1 CDC---RGDCFC 9
DB 75 CDCCGERGECVC 86

RESULT 11

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CC -----
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CC -----
DR EMBL; AF014464; AAC26166.1; -.
KW Sodium channel inhibitor; Toxin; Neurotoxin; Ionic channel inhibitor;
KW Signal.
FT SIGNAL. 1 17 POTENTIAL.
FT PROPEP 18 34 BY SIMILARITY.
FT CHAIN 35 87 NEUROTOXIN TX2-1.
FT PROPEP 88 88 BY SIMILARITY.
SQ SEQUENCE 88 AA; 9841 MW; D8AD07C6A769E647 CRC64;

Query Match 65.4%; Score 42.5; DB 1; Length 88;
Best Local Similarity 58.3%; Pred. No. 2;
Matches 7; Conservative 1; Mismatches 1; Indels 3; Gaps 1;

QY 1 CDC---RGDCFC 9
DB 48 CDCCGERGECVC 59

RESULT 10
TX1A_PHONI
ID TX1A PHONI STANDARD; PRT; 115 AA.
AC O76198;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neurotoxin Pn2-1A precursor.
OS Phoneutria nigriventer (Brazilian armed spider).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
OC Araneomorphae; Entelegynae; Lycosoidea; Ctenidae; Phoneutria.
OX NCBI_TaxID=6918;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RX MEDLINE=99053403; PubMed=9839668;
RA Kalapothakis E., Penaforte C.L., Beirao P.S.L., Romano-Silva M.A.,
RA Cruz J.S., Prado M.A.M., Guimaraes P.E.M., Gomez M.V., Prado V.F.;
RA "Cloning of cDNAs encoding neurotoxic peptides from the spider
RT Phoneutria nigriventer.";
RT Toxicon 36:1843-1850(1998).
RN [2]
RP SEQUENCE OF 35-87.
RC TISSUE=Venom;
RX MEDLINE=93011905; PubMed=1397265;
RA Cordeliro M.N., Diniz C.R., Valentim A.D.C., von Eickstedt V.R.D.,
RA Gilroy J., Richardson M.;
RT "The purification and amino acid sequences of four Tx2 neurotoxins
RT from the venom of the Brazilian 'armed' spider Phoneutria nigriventer
RT (Keys).";
RL FEBS Lett. 310:153-156(1992).
CC -!- FUNCTION: Blocks voltage-gated sodium channels (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -!- SIMILARITY: Belongs to the spider toxin Tx2 family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF014462; AAC26164.1; -.
KW Sodium channel inhibitor; Toxin; Neurotoxin; Ionic channel inhibitor;
KW Signal.
FT SIGNAL. 1 17 POTENTIAL.
FT PROPEP 18 61 BY SIMILARITY.
FT CHAIN 62 114 NEUROTOXIN PN2-1A.
FT PROPEP 115 115 BY SIMILARITY.
FT PROPEP 115 115 BY SIMILARITY.
SQ SEQUENCE 115 AA; 12858 MW; B7D321750F7BA50 CRC64;

Query Match 65.4%; Score 42.5; DB 1; Length 115;
Best Local Similarity 58.3%; Pred. No. 2;
Matches 7; Conservative 1; Mismatches 1; Indels 3; Gaps 1;

QY 1 CDC---RGDCFC 9
DB 75 CDCCGERGECVC 86

RESULT 11

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CRS5_YEAST
ID CRS5_YEAST STANDARD; PRT; 69 AA.
AC P41902;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Metallothionein-like protein CRS5.
DE CRS5 OR YOR031W.
GN
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95014318; PubMed=7929222;
RA Culotta V.C., Howard W.R., Liu X.F.;
RT "CRS5 encodes a metallothionein-like protein in Saccharomycetes
RT cerevisiae."
RL J. Biol. Chem. 269:25295-25302(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288c / Fy1679;
RA de Haan M., Maarse A.C., Grivell L.A.;
RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Critical role in copper (specific) homeostasis and
CC detoxification. May protect by directly chelating and sequestering
CC copper ions.
CC -!- SIMILARITY: BELONGS TO THE METALLOTHIONEIN SUPERFAMILY; FAMILY 13.
CC
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CC
CC -----
DR EMBL; L29056; AAA66061.1; -.
DR EMBL; X87331; -. NOT ANNOTATED_CDS.
DR PIR; A55011; A55011.
DR GERMOnline; 143619; -.
DR SGD; S0005557; CRS5.
DR GO; GO:0005507; F:copper ion binding; IMP.
DR GO; GO:0010038; P:response to metal ion; IMP.
DR InterPro; IPR002400; GF_cysknot.
DR PRINTS; PR00438; GFCYSKNOT.
DR KW Metal-binding; Metal-thiolate cluster; Copper.
SQ SEQUENCE 69 AA; 7321 MW; CEEF91203A813FF4 CRC64;

Query Match 63.1%; Score 41; DB 1; Length 69;
Best Local Similarity 71.4%; Pred.No. 2.9;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CDCRGDC 7
||| |.
Db 6 CDCEGEC 12

RESULT 12
LML2_CAEEL STANDARD; PRT; 3672 AA.
AC Q2133;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Laminin-like protein K08C7.3 precursor.
GN K08C7.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodirinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN=Bristol N2;
RA Berks M.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 1 laminin N-terminal domain.
CC -!- SIMILARITY: Contains 22 laminin EGF-like domains.
CC -!- SIMILARITY: Contains 1 laminin IV domain.
CC -!- SIMILARITY: Contains 5 laminin G-like domains.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC
CC -----
DR EMBL; Z70286; CAA94293.1; -.
DR PIR; T23433; T23433.
DR HSSP; P02468; 1KLO.
DR WormPep; K08C7.3; CE061136.
DR InterPro; IPR008985; ConA_like_lect_gl.
DR InterPro; IPR006209; EGF_Like.
DR InterPro; IPR000334; Laminin B.
DR InterPro; IPR002049; Laminin EGF.
DR InterPro; IPR001791; Laminin G.
DR InterPro; IPR008211; LamNT.
DR Pfam; PF00052; laminin_B; 1.
DR Pfam; PF00053; laminin_Egf; 20.
DR Pfam; PF00054; laminin_G; 5.
DR Pfam; PF00055; laminin_Nterm; 1.
DR PRINTS; PR00011; EGFLAMININ.
DR SMART; SM00180; EGF_Lam; 17.
DR SMART; SM00281; LamB; 1.
DR SMART; SM00282; LamG; 5.
DR SMART; SM00136; LamNT; 1.
DR PROSITE; PS00022; EGF_1; 19.
DR PROSITE; PS01186; EGF_2; 4.
DR PROSITE; PS01248; LAMININ TYPE EGF; 21.
DR PROSITE; PS00025; LAM_G DOMAIN; 5.
KW Hypothetical protein; Laminin EGF-like domain; Signal; Repeat.
FT SIGNAL 1 27 POTENTIAL.
FT CHAIN 28 3672 LAMININ-LIKE PROTEIN K08C7.3.
FT DOMAIN 28 297 LAMININ N-TERMINAL (DOMAIN VI).
FT DOMAIN 298 356 LAMININ EGF-LIKE 1.
FT DOMAIN 357 426 LAMININ EGF-LIKE 2.
FT DOMAIN 427 471 LAMININ EGF-LIKE 3.
FT DOMAIN 472 518 LAMININ EGF-LIKE 4.
FT DOMAIN 519 563 LAMININ EGF-LIKE 5.
FT DOMAIN 564 609 LAMININ EGF-LIKE 6.
FT DOMAIN 610 655 LAMININ EGF-LIKE 7.
FT DOMAIN 656 700 LAMININ EGF-LIKE 8.
FT DOMAIN 701 755 LAMININ EGF-LIKE 9.
FT DOMAIN 756 808 LAMININ EGF-LIKE 10.
FT DOMAIN 809 839 LAMININ EGF-LIKE 11 (INCOMPLETE).
FT DOMAIN 1415 1460 LAMININ EGF-LIKE 12.
FT DOMAIN 1461 1505 LAMININ EGF-LIKE 13.
FT DOMAIN 1506 1553 LAMININ EGF-LIKE 14.
FT DOMAIN 1554 1604 LAMININ EGF-LIKE 15.
FT DOMAIN 1605 1614 LAMININ EGF-LIKE 16 (N-TERMINAL).
FT DOMAIN 1615 1796 LAMININ DOMAIN IV.
FT DOMAIN 1797 1829 LAMININ EGF-LIKE 16 (C-TERMINAL).
FT DOMAIN 1830 1879 LAMININ EGF-LIKE 17.
FT DOMAIN 1880 1936 LAMININ EGF-LIKE 18.
FT DOMAIN 1937 1989 LAMININ EGF-LIKE 19.
FT DOMAIN 1990 2036 LAMININ EGF-LIKE 20.
FT DOMAIN 2037 2083 LAMININ EGF-LIKE 21.
FT DOMAIN 2084 2131 LAMININ EGF-LIKE 22.
FT DOMAIN 2693 2884 LAMININ G-LIKE 1.
FT DOMAIN 2886 3066 LAMININ G-LIKE 2.
FT DOMAIN 3072 3235 LAMININ G-LIKE 3.
FT DOMAIN 3310 3482 LAMININ G-LIKE 4.
FT DOMAIN 3488 3669 LAMININ G-LIKE 5.
FT DISULFID 298 307 BY SIMILARITY.

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FT DISULFID 300 BY SIMILARITY.
FT DISULFID 322 BY SIMILARITY.
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FT DISULFID 585 BY SIMILARITY.
FT DISULFID 597 BY SIMILARITY.
FT DISULFID 610 BY SIMILARITY.
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FT DISULFID 1415 BY SIMILARITY.
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FT DISULFID 1554 BY SIMILARITY.
FT DISULFID 1556 BY SIMILARITY.
FT DISULFID 1575 BY SIMILARITY.
FT DISULFID 1587 BY SIMILARITY.
FT DISULFID 1830 BY SIMILARITY.
FT DISULFID 1832 BY SIMILARITY.
FT DISULFID 1849 BY SIMILARITY.
FT DISULFID 1861 BY SIMILARITY.
FT DISULFID 1877 BY SIMILARITY.
FT DISULFID 1880 BY SIMILARITY.
FT DISULFID 1882 BY SIMILARITY.
FT DISULFID 1907 BY SIMILARITY.
FT DISULFID 1916 BY SIMILARITY.
FT DISULFID 1919 BY SIMILARITY.
FT DISULFID 1937 BY SIMILARITY.
FT DISULFID 1939 BY SIMILARITY.
FT DISULFID 1958 BY SIMILARITY.
FT DISULFID 1961 BY SIMILARITY.
FT DISULFID 1973 BY SIMILARITY.
FT DISULFID 1987 BY SIMILARITY.
FT DISULFID 1990 BY SIMILARITY.
FT DISULFID 1992 BY SIMILARITY.
FT DISULFID 2009 BY SIMILARITY.
FT DISULFID 2021 BY SIMILARITY.
FT DISULFID 2034 BY SIMILARITY.
FT DISULFID 2037 BY SIMILARITY.
FT DISULFID 2048 BY SIMILARITY.
FT DISULFID 2055 BY SIMILARITY.

FT DISULFID 2057 2066 BY SIMILARITY.
FT DISULFID 2069 2081 BY SIMILARITY.
FT DISULFID 2084 2096 BY SIMILARITY.
FT DISULFID 2086 2103 BY SIMILARITY.
FT DISULFID 2105 2114 BY SIMILARITY.
FT DISULFID 2117 2129 BY SIMILARITY.
FT CARBOHYD 121 121 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 140 140 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 140 140 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 249 249 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 351 351 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 477 477 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 511 511 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 530 530 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 634 634 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 761 761 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1014 1014 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1341 1341 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1705 1705 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1756 1756 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1868 1868 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1944 1944 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1986 1986 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 2002 2002 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 2159 2159 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 2207 2207 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 2231 2231 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 2235 2235 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 2401 2401 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 2421 2421 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 2487 2487 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 2821 2821 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 3087 3087 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 3242 3242 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 3541 3541 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 3672 AA; 404223 MW; 28E262DB5FF14BFA CRC64;

Query Match 63.1%; Score 41; DB 1; Length 3672;
Best Local Similarity 55.6%; Pred. No. 1.2e-02;

Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CDCRGDCPC 9
Db 668 CDSNGQCYC 676

RESULT 13

ID ITEN_DROME STANDARD; PRT; 799 AA.
AC Q27591; Q9VIG7;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Integrin beta-nu precursor.
GN BETA-INT-NU OR CGI762.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Midgut endoderm;
RC MEDLINE=94357079; PubMed=8076521;
RA Yee G.H., Hynes R.O.;
RT "A novel, tissue-specific integrin subunit, beta nu, expressed in the
midgut of Drosophila melanogaster.";
RL Development 118:845-858(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RC MEDLINE=20196006; PubMed=10731132;
RX Adams M.D., Celnikier S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 Branton R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 Beeson K.D., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 Burtis K.C., Buesam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 Foster C., Gong F., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 Jalali M., Kalush F., Karen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 Laoko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Paclab J.M.,
 Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 Shue B.C., Siden-Klamis I., Simpson M., Skupski M.P., Smith T.,
 Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
 Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 Gibbs R.H., Myers E.W., Rubin G.M., Venter J.C.;
 "The genome sequence of *Drosophila melanogaster*.";
 Science 287:2185-2195(2000).
 CC -!- FUNCTION: PROBABLY PLAYS A ROLE IN CELL ADHESION.
 CC -!- SUBUNIT: Heterodimer of an alpha and a beta subunit.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: Belongs to the integrin beta chain family.
 CC -!- SIMILARITY: Contains 1 VWFA domain.
 CC -----
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 CC -----
 CC EMBL; L13305; AAC37169.1; -;
 CC EMBL; AE003669; AAF53952.1; -;
 CC HSPSP; P05106; IJY2.
 CC -----
 CC Flybase; FBgn0010395; beta-Int-nu.
 CC InterPro; IPR006209; EGF-like.
 CC InterPro; IPR002369; Integrin_B.
 CC InterPro; IPR001169; Integrin_beta_C.
 CC InterPro; IPR002049; Laminin_EGF.
 CC InterPro; IPR003659; Plexin-like.
 CC InterPro; IPR002035; VWFA.
 CC Pfam; PF00362; integrin_B; 1.
 CC PRINTS; PR00011; EGF_LAMININ.
 CC ProDom; PD001811; Integrin.
 CC ProDom; PD001811; Integrin_B; 1.
 CC SMART; SM00187; INB; 1.
 CC SMART; SM00423; PSI; 1.
 CC SMART; SM00327; VWA; 1.
 CC PROSITE; PS00022; EGF_1; UNKNOWN 4.
 CC PROSITE; PS01186; EGF_2; UNKNOWN 4.
 CC PROSITE; PS00243; INTEGRIN_BETA; 1.
 CC PROSITE; PS02034; VWFA; 1.
 CC PROSITE; PS50076; Dnaj_2; FALSE_NEG.
 CC Integrin; Cell adhesion; Receptor; Transmembrane; Glycoprotein;
 Signal.

FT SIGNAL 1 26 POTENTIAL.
 FT CHAIN 27 799 INTEGRIN BETA-NU.
 FT DOMAIN 27 795 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 726 746 POTENTIAL.
 FT DOMAIN 747 799 POTENTIAL.
 FT DOMAIN 136 372 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 73 73 VWFA.
 FT CARBOHYD 167 167 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 409 409 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 505 505 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 655 655 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 680 701 E -> G (IN REF. 1).
 FT CONFLICT 701 701 V -> A (IN REF. 1).
 SQ SEQUENCE 799 AA; 90841 MW; 351869D523F07DEB CRC64;
 Query Match 62.3%; Score 40.5; DB 1; Length 799;
 Best Local Similarity 38.9%; Pred No. 35;
 Matches 7; Conservative 1; Mismatches 1; Indels 9; Gaps 1;
 QY 1 CPCR-----GDCFC 9
 Db 552 CECRECLDCDEKLADCF 569
 RESULT 14
 TASM_FOVMA STANDARD; PRT; 195 AA.
 ID TASM_FOVMA AC P03078;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Small T antigen.
 OS Mouse polyomavirus (strain A2), and
 OS Mouse polyomavirus (strain 3).
 OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
 OX NCBI_TaxID=10636, 10635;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A2;
 RX MEDLINE=80099647; PubMed=6243401;
 RA Soeda E., Arrand J.R., Smolar N., Walsh J.E., Griffin B.E.;
 RT "Coding potential and regulatory signals of the polyoma virus
 RT genome.";
 RL Nature 283:445-453(1980).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=3;
 RX MEDLINE=80001963; PubMed=225042;
 RA Friedmann T., Esty A., Laporte P., Deininger P.L.;
 RT "The nucleotide sequence and genome organization of the polyoma early
 RT region: extensive nucleotide and amino acid homology with SV40.";
 RL Cell 17:715-724(1979).
 CC -!- SIMILARITY: Contains 1 J domain.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; J02289; AAA46874.1; -;
 CC EMBL; J02288; AAB59899.1; -;
 CC PIR; C03635; TVVPA.
 CC InterPro; IPR001623; DnaJ_N.
 CC InterPro; IPR003354; Papo_T_antigen.
 CC Pfam; PF00226; DnaJ; 1.
 CC Pfam; PF02380; Papo_T_antigen; 1.
 CC SMART; SM00271; DnaJ; 1.
 CC PROSITE; PS00636; DnaJ_1; FALSE_NEG.
 CC PROSITE; PS50076; DnaJ_2; FALSE_NEG.
 CC Early protein.

FT DOMAIN 12 75 J-DOMAIN.
SQ SEQUENCE 195 AA; 22811 MW; 44EED6711E1AFEC3 CRC64;
Query Match 61.5%; Score 40; DB 1; Length 195;
Best Local Similarity 53.8%; Pred. No. 11;
Matches 7; Conservative 1; Mismatches 1; Indels 4; Gaps 1;

QY 1 CDCR----GDCFC 9
||| :|||
Db 138 CDARCLVLGECFC 150

RESULT 15
TAMI_POVNA
ID TAMI_POVNA STANDARD; PRT; 421 AA.
AC P03077;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Middle T antigen.
OS Mouse polyomavirus (strain A2).
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10636;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=80099647; PubMed=6243401;
RA Soeda E., Arrand J.R., Smolar N., Walsh J.E., Griffin B.E.;
RT "Coding potential and regulatory signals of the polyoma virus genome."
RL Nature 283:445-453(1980).
CC -!- SIMILARITY: Contains 1 J domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
CC EMBL; J02288; AAS59900.1; .
DR InterPro; IPR001623; DnaJ_N.
DR InterPro; IPR003354; Papo_T_antigen.
DR Pfam; PF00226; DnaJ; 1.
DR Pfam; PF02380; Papo_T_antigen; 1.
DR SMART; SM00271; DnaJ; 1.
DR PROSITE; PS00636; DnaJ_1; FALSE_NEG.
DR PROSITE; PS50076; DnaJ_2; FALSE_NEG.
KW Early protein.
FT DOMAIN 12 75 J-DOMAIN.
SQ SEQUENCE 421 AA; 48622 MW; CAOC25C4984CACB7 CRC64;

Query Match 61.5%; Score 40; DB 1; Length 421;
Best Local Similarity 53.8%; Pred. No. 23;
Matches 7; Conservative 1; Mismatches 1; Indels 4; Gaps 1;

QY 1 CDCR----GDCFC 9
||| :|||
Db 138 CDARCLVLGECFC 150

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 11, 2004, 09:14:02 ; Search time 39 Seconds
(without alignments)
72.812 Million cell updates/sec

Title: US-09-734-628-1

Perfect score: 65

Sequence: 1 CDCRGDCFC 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriaph:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	69.2	676	10 Q861X3	Q861X3 oryza sativ
2	45	69.2	696	10 Q8L821	Q8L821 zea mays (m
3	44	67.7	114	11 Q91511	Q91511 cavia porce
4	44	67.7	439	16 Q87QB5	Q87QB5 vibrio para
5	44	67.7	787	6 Q863C4	Q863C4 ovis aries
6	44	67.7	788	5 Q8SQB8	Q8SQB8 bos taurus
7	43	66.2	954	5 Q9GYG8	Q9GYG8 caenorhabdi
8	42	64.6	463	10 Q9C599	Q9C599 arabidopsis
9	41	63.1	74	5 Q8WQ95	Q8WQ95 crassostrea
10	41	63.1	218	10 Q851N3	Q851N3 oryza sativ
11	41	63.1	458	17 Q9HRQ4	Q9HRQ4 halobacteri
12	41	63.1	535	4 Q96EB1	Q96EB1 homo sapien
13	41	63.1	546	12 Q80IB8	Q80IB8 influenza a
14	41	63.1	549	12 Q80IA8	Q80IA8 influenza a
15	41	63.1	552	12 Q80IC9	Q80IC9 influenza a
16	41	63.1	552	12 Q80IC5	Q80IC5 influenza a

17	41	63.1	552	12 Q80IB9	Q80IB9 influenza a
18	41	63.1	552	12 Q80IB7	Q80IB7 influenza a
19	41	63.1	552	12 Q80IA1	Q80IA1 influenza a
20	41	63.1	552	12 Q80I97	Q80I97 influenza a
21	41	63.1	552	12 Q80I95	Q80I95 influenza a
22	41	63.1	552	12 Q80I82	Q80I82 influenza a
23	41	63.1	736	10 Q9SVX7	Q9SVX7 arabidopsis
24	41	63.1	1162	5 Q8WTP0	Q8WTP0 halocynthia
25	41	63.1	3704	5 P91904	P91904 caenorhabdi
26	40	61.5	100	5 Q962G0	Q962G0 littorina l
27	40	61.5	116	12 Q9IBN0	Q9IBN0 polyomaviru
28	40	61.5	119	12 Q84251	Q84251 polyomaviru
29	40	61.5	167	12 Q84326	Q84326 polyomaviru
30	40	61.5	195	11 Q04190	Q04190 mus musculu
31	40	61.5	196	12 Q8V9F4	Q8V9F4 murine poly
32	40	61.5	211	12 Q84854	Q84854 polyomaviru
33	40	61.5	214	12 Q84252	Q84252 polyomaviru
34	40	61.5	313	5 Q24330	Q24330 dictyosteli
35	40	61.5	320	5 Q721Y7	Q721Y7 loxosceles
36	40	61.5	365	16 Q81QZ7	Q81QZ7 bacillus an
37	40	61.5	421	11 Q04188	Q04188 mus musculu
38	40	61.5	421	12 Q89765	Q89765 murine poly
39	40	61.5	494	11 Q9QZB6	Q9QZB6 mus musculu
40	40	61.5	625	10 Q9LP82	Q9LP82 arabidopsis
41	40	61.5	677	13 Q7SZW3	Q7SZW3 brachydanio
42	40	61.5	690	13 Q7ZYI6	Q7ZYI6 brachydanio
43	40	61.5	711	13 Q7ZYI8	Q7ZYI8 brachydanio
44	40	61.5	729	13 Q7SZW2	Q7SZW2 brachydanio
45	40	61.5	768	13 Q98TH8	Q98TH8 cyprinus ca

ALIGNMENTS

RESULT 1

Q851X3	PRELIMINARY;	PRT;	676 AA.
ID	Q851X3		
AC	Q851X3		
DT	01-JUN-2002 (TREMELrel. 21, Created)		
DT	01-JUN-2002 (TREMELrel. 21, Last sequence update)		
DT	01-JUN-2003 (TREMELrel. 24, Last annotation update)		
DE	Putative SUVH4.		
GN	P0482D04.21 OR OSJNBA0093F16.17.		
OS	Oryza sativa (japonica cultivar-group).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;		
OC	Ehrhartoideae; Oryzaceae; Oryza.		
OX	NCBI_TaxID=39947;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=cv. Nipponbare;		
RA	Sasaki T., Matsumoto T., Yamamoto K.;		
RT	"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC		
RT	clone:P0482D04.21";		
RL	Submitted (FEB-2001) to the EMBL/GenBank/DBSJ databases.		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=cv. Nipponbare;		
RA	Sasaki T., Matsumoto T., Yamamoto K.;		
RT	"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, BAC		
RT	clone:OSJNBA0093F16.17";		
RL	Submitted (NOV-2001) to the EMBL/GenBank/DBSJ databases.		
DR	EMBL; AF003262; BAB9674.1; -		
DR	EMBL; AF004332; BAB92897.1; -		
DR	Genbank; Q851X3; -		
DR	InterPro; IPR003105; G9a.		
DR	InterPro; IPR003616; PostSET.		
DR	InterPro; IPR007726; Pre-SET.		
DR	InterPro; IPR001214; SET.		
DR	Pfam; PF05033; Pre-SET; 1.		
DR	Pfam; PF00856; SET; 1.		
DR	Pfam; PF02182; YDG SRA; 1.		
DR	PROSITE; PS50568; POST_SET; 1.		

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DR PROSITE; PS50867; PRE-SET; 1.
DR PROSITE; PS50280; SET; 1.
SQ SEQUENCE 676 AA; 74816 MW; 93677BDC449DCFE68 CRC64;

Query Match 69.2%; Score 45; DB 10; Length 676;
Best Local Similarity 85.7%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CDCRGDC 7
DB 435 CDCGDC 441

RESULT 2
Q8L821 PRELIMINARY; PRT; 696 AA.
AC Q8L821
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE SET domain-containing protein SET118.
GN SET118.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. B73;
RA Chandler V.L., Kaeppler S.M., Kaeppler H.F., Cone K.C.;
RT "Sequences from the Plant Chromatin Consortium (NSF Plant Genome
Program Grant 9975930).";
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. B73;
RA Bergstrom D.E., Springer N.M., Schmitt L.T., Guthrie E., Sidorenko L.,
RA Selinger D., Kaeppler S.M., Cone K.C.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: CONTAINS 1 SET DOMAIN.
DR EMBL; AY122271; AAM89287.1; -.
DR InterPro; IPR003105; G9a.
DR InterPro; IPR003616; PostSET.
DR InterPro; IPR007728; Pre-SET.
DR InterPro; IPR001214; SET.
DR InterPro; IPR003606; Zn2-binding.
DR Pfam; PF05033; Pre-SET; 1.
DR Pfam; PF00856; SET; 1.
DR Pfam; PF02182; YDG_SRA; 1.
DR SMART; SM00508; PostSET; 1.
DR SMART; SM00468; PreSET; 1.
DR SMART; SM00317; SET; 1.
DR SMART; SM00466; SRA; 1.
DR PROSITE; PS50868; POST-SET; 1.
DR PROSITE; PS50867; PRE-SET; 1.
DR PROSITE; PS50280; SET; 1.
SQ SEQUENCE 696 AA; 76861 MW; 6F30A9018126C9AD CRC64;

Query Match 69.2%; Score 45; DB 10; Length 696;
Best Local Similarity 85.7%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CDCRGDC 7
DB 455 CDCGDC 461

RESULT 3
Q9R151 PRELIMINARY; PRT; 114 AA.
ID Q9R151
AC Q9R151
DT 01-MAY-2000 (TReMBLrel. 13, Created)

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DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Integrin beta 6 (Fragment).
OC Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Hartley; TISSUE=Trachea;
RA Morishima Y., Uchida Y., Nomura A., Ishii Y., Sakamoto T.,
RA Sekizawa K.;
RT "Guinea-pig beta-6 integrin expression in injured tracheal
epithelium.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF169344; AAD49344.1; -.
DR HSP; P05106; 1JV2.
DR GO; GO:0008305; C: integrin complex; IEA.
DR GO; GO:0004895; F: cell adhesion receptor activity; IEA.
DR GO; GO:0007160; P: cell-matrix adhesion; IEA.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR002369; Integrin_B.
DR Pfam; PF00362; Integrin_B; 1.
DR ProDom; PD001811; Integrin_B; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR NON_TER 1
FT NON_TER 114
FT NON_TER 114
SQ SEQUENCE 114 AA; 12121 MW; 95D4528EBD0435EF CRC64;

Query Match 67.7%; Score 44; DB 11; Length 114;
Best Local Similarity 66.7%; Pred. No. 4.3;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CDCRGDCFC 9
DB 104 CSGRGDCYC 112

RESULT 4
Q87QB5 PRELIMINARY; PRT; 439 AA.
AC Q87QB5
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Iron-containing alcohol dehydrogenase.
GN VP1235.
OS Vibrio parahaemolyticus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=670;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RIMD 2210633 / Serotype O3:K6;
RX MEDLINE=22508454; PubMed=12620739;
RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
RA Iijima Y., Nakano M., Yamashita A., Kubota Y., Kimura S.,
RA Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
RT "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
distinct from that of V. cholerae.";
RL Lancet 361:743-749 (2003).
DR EMBL; AP005072; BAC59498.1; -.
DR GO; GO:000506; F: iron ion binding; IEA.
DR GO; GO:0016491; F: oxidoreductase activity; IEA.
DR GO; GO:0008152; P: metabolism; IEA.
DR InterPro; IPR001670; Fe-ADH.
DR Pfam; PF00465; Fe-ADH; 1.
DR Complete proteome.
SQ SEQUENCE 439 AA; 47354 MW; BALA035739CF1953 CRC64;

Query Match 67.7%; Score 44; DB 16; Length 439;
Best Local Similarity 85.7%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY      1 CDCRGDC 7
Db      408 CDCGDC 414

RESULT 5
Q863C4 PRELIMINARY; PRT; 787 AA.
AC Q863C4;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Integrin subunit beta-6 (fragment).
GN ITB6.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Upper airway;
RA McAleese S.M., Collie D.D.S., Miller H.R.P.;
RT "Cloning and sequencing of the cDNA for sheep integrin subunit beta-
6".
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ43962; CAD27749.1; -.
DR GO; GO:0008305; C:integrin complex; IEA.
DR GO; GO:0004895; F:cell adhesion receptor activity; IEA.
DR GO; GO:0007160; P:cell-matrix adhesion; IEA.
DR GO; GO:0007275; P:development; IEA.
DR GO; GO:0007229; P:integrin-mediated signaling pathway; IEA.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR002369; Integrin_B.
DR InterPro; IPR001169; Integrin_beta_C.
DR InterPro; IPR003659; Plexin-like.
DR Pfam; PF00362; integrin_B; 1.
DR PRINTS; PR01186; INTEGRINB.
DR ProDom; PD001811; Integrin_B; 1.
DR SMART; SM00187; INB; 1.
DR SMART; SM00423; PSI; 1.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS00022; EGF_1; 2.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS00243; INTEGRIN_BETA; 2.
KW Cell adhesion; Glycoprotein; Integrin; Repeat; Signal; Transmembrane.
FT SIGNAL 1 26
FT CHAIN 27 788 INTEGRIN BETA 6 SUBUNIT.
SQ SEQUENCE 788 AA; 85892 MW; FB9B5197BFF56EEB CRC64;

Query Match 67.7%; Score 44; DB 6; Length 788;
Best Local Similarity 66.7%; Pred. No. 21;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 CDCRGDCFC 9
Db      511 CSGRGDCYC 519

RESULT 7
Q9GYG8 PRELIMINARY; PRT; 954 AA.
AC Q9GYG8;
DT 01-WAR-2001 (TrEMBLrel. 16, Created)
DT 01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN W01C8.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Nham M.;
RT "The sequence of C. elegans cosmid W01C8.";
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;

```

RA Waterston R.;
 RT "Direct Submission."
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS 1 SET DOMAIN.
 DE EMBL; U41508; AGO0027.2; -.
 DR WormPep; W01C8.3; CE30196.
 DR InterPro; IPR001214; SET.
 DR Pfam; PF00856; SET; 1.
 DR SMART; SM00317; SET; 1.
 DR PROSITE; PS50280; SET; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 954 AA; 107835 MW; E7747E40ADD941B6 CRC64;

Query Match 66.2%; Score 43; DB 5; Length 954;
 Best Local Similarity 85.7%; Pred. No. 36;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CDCRGDC 7

Db 144 CGCRGDC 150

RESULT 8

Q9C599 PRELIMINARY; PRT; 463 AA.

AC Q9C599
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 GN AT5G08780.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OC NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bevan M., Murphy G., Ridley P., Hudson S., Bancroft I., Mewes H.W.,
 RA Rudd S., Lemcke K., Mayer K.F.X.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DE EMBL; AL590346; CAC35893.1; -.
 DR HSP; P02259; IHS1.
 DR GO; GO:000786; C:nucleosome; IEA.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR GO; GO:0007001; P:nucleosome organization and biogenesis (sen. .; IEA.
 DR GO; GO:0006334; P:nucleosome assembly; IEA.
 DR InterPro; IPR005818; Histone_H1/H5.
 DR InterPro; IPR003216; LinkerHist_N.
 DR Pfam; PF00538; LinkerHistone; I.
 DR ProDom; PD000373; LinkerHist_N; 1.
 DR SMART; SM00526; H15; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 463 AA; 52015 MW; 781A08F0BB11DCAA CRC64;

Query Match 64.6%; Score 42; DB 10; Length 463;
 Best Local Similarity 62.5%; Pred. No. 29;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CDCRGDC 8

Db 114 CDCNNDY 121

RESULT 9

Q8WQ95 PRELIMINARY; PRT; 74 AA.
 ID Q8WQ95
 AC Q8WQ95;

DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Metallothionein (Fragment).
 GN MT3.
 OS Crassostrea gigas (Pacific oyster).
 OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Ostreoida;
 OC Ostreoida; Ostreidae; Crassostrea.
 NCBI_TaxID=29159;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Tissue=Gill.
 RA Tanguy A., Boutet I., Moraga D.;
 RT "Cloning and characterization of a third metallothionein gene in the
 RT Pacific oyster Crassostrea gigas: a singular case."
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 DE EMBL; AJ295157; CAC82788.1; -.
 DR GO; GO:0046872; F:metal ion binding; IEA.
 DR InterPro; IPR003019; Metallothion_2.
 DR InterPro; IPR001008; Metallothion_2.
 DR Pfam; PF00131; metalthio; 1.
 DR PRINTS; PR00875; MTMOLLUSC.
 FT NON TER 1
 SQ SEQUENCE 74 AA; 7274 MW; 5D9DD049577B74AE CRC64;

Query Match 63.1%; Score 41; DB 5; Length 74;
 Best Local Similarity 55.6%; Pred. No. 9.3;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CDCRGDCFC 9

Db 46 CNCNGSCAC 54

RESULT 10

Q851N3 PRELIMINARY; PRT; 218 AA.
 AC Q851N3
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Hypothetical protein.
 GN OSJNBA0042109.11.
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzeae; Oryza.
 NCBI_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Nipponbare;
 RA Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M.,
 RA Overton II L.L., Tsitrin T., Kim M.M., Bera J.J., Jin S.S.,
 RA Padrosh D.W., Tallon L.J., Koo H., Zismann V., Hsiao J., Blunt S.,
 RA Vanaken S.S., Riedmuller S.B., Utterback T.T., Feldblyum T.V.,
 RA Yang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J.,
 RA White O., Salzberg S.L., Fraser C.M.;
 RT "Oryza sativa chromosome 3 BAC OSJNBA0042109 genomic sequence."
 RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
 DE EMBL; AC104487; AAO41141.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 218 AA; 24562 MW; 4FE0A501A4A17507 CRC64;

Query Match 63.1%; Score 41; DB 10; Length 218;
 Best Local Similarity 100.0%; Pred. No. 23;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DCRGDC 7

Db 202 DCRGDC 207

RESULT 11

Q9HPQ4	PRELIMINARY; PRT; 458 AA.
ID	Q9HPQ4
AC	Q9HPQ4
DT	01-MAR-2001 (TrEMBLrel. 16, Created)
DT	01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE	Vng1524C.
DE	Vng1524C.
GN	VNG1524C.
OS	Halobacterium sp. (strain NRC-1 / ATCC 700922 / JCM 11081).
OC	Archaea; Euryarchaeota; Halobacteriia; Halobacteriales;
OC	Halobacteriaceae; Halobacterium.
NCBI_TaxID=64091;	
OX	NCBI_TaxID=64091;
RN	[1]
RP	SEQUENCE FROM N.A.
RP	SEQUENCE FROM N.A.
EX	MEDLINE=20504483; PubMed=11016950;
RA	Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
RA	Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
RA	Shukla H.D., Laskey S.R., Balliga N.S., Thorsson V., Shrogha J.,
RA	Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
RA	Leithausser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
RA	Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
RA	Isebnacker T.A., Peck R.F., Pohlschroder M., Spudis J.L., Jung K.-H.,
RA	Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
RA	Ehardt H., Lowe T.M., Liang P., Riley M., Hood L., Dassarma S.,
RT	"Genome sequence of Halobacterium species NRC-1."
RL	Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
DR	EMBL; AE005065; AAG19813.1; -.
DR	PUR; A84306; A84306
DR	GO; GO:0008483; P:transaminase activity; IEA.
DR	InterPro; IPR005814; AminoTrans_3.
DR	InterPro; IPR001220; Lectin_leg3.
DR	Pfam; PF00202; aminotran_3; 1.
DR	PROSITE; PS00600; AA TRANSFER CLASS 3; 1.
DR	PROSITE; PS00307; LECTIN_LEGUME_BETA; 1.
KW	Complete proteome.
QY	SEQUENCE 458 AA; 49439 MW; BLEA7132978E0F0E CRC64;
QY	1 CDCRGDCFC 9
Db	198 CTCEGCSC 206
Query Match	63.1%; Score 41; DB 17; Length 458;
Best Local Similarity	55.6%; Pred.No. 42;
Matches	5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
RESULT 12	
Q96EB1	PRELIMINARY; PRT; 535 AA.
ID	Q96EB1
AC	Q96EB1
DT	01-DEC-2001 (TrEMBLrel. 19, Created)
DT	01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE	Similar to hypothetical protein.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;	
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RP	TISSUE=Testis, and Embryonic carcinoma;
RA	Strausberg R.
RL	Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR	EMBL; BC012514; AAH12514.1; -.
DR	Genew; HGNC:1171; ELP4.
DR	InterPro; IPR008728; FAXNEB.
DR	Pfam; PF05625; FAXNEB; 1.
QY	SEQUENCE 535 AA; 58713 MW; 86E6DD3B545E96D4 CRC64;
QY	3 CRGDCFC 9
Query Match	63.1%; Score 41; DB 4; Length 535;
Best Local Similarity	71.4%; Pred.No. 47;
Matches	5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 CRGDCF 8
 Db 275 CRGDCF 280

RESULT 15

Q801C9 PRELIMINARY; PRT: 552 AA.

AC Q801C9;
 DT 01-JUN-2003 (TREMELrel. 24, Created)
 DT 01-JUN-2003 (TREMELrel. 24, Last sequence update)
 DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
 DE Hemagglutinin.
 OS Influenza A virus (A/avian/NY/70411-12/00 (H7N2)).
 OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
 OC Influenza A viruses; Influenzavirus A.
 CX NCBI_TaxID=226617;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A/Avian/NY/70411-12/00;
 RA Spackman E., Suarez D.L., Senne D.A., Davison S.;
 RT "Sequence Analysis of Recent H7 Avian Influenza Viruses Associated
 RT with Three Different Outbreaks in Commercial Poultry in the US.";
 RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY240878; AAC86905.1; -
 DR InterPro; IPR008980; Capsid hemag.
 DR InterPro; IPR001364; Hemagglutn.
 DR Pfam; PF00509; Hemagglutinin; 1.
 DR PRINTS; PR00329; HEMAGGLUTN12.
 DR PRODOM; PD000225; Hemagglutn; 1.
 SQ SEQUENCE 552 AA; 61407 MW; C80AD822D34B5C54 CRC64;

Query Match 63.1%; Score 41; DB 12; Length 552;
 Best Local Similarity 100.0%; Pred. No. 49;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CRGDCF 8
 Db 278 CRGDCF 283

Search completed: July 11, 2004, 09:14:58
 Job time : 42 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: July 11, 2004, 09:14:02 ; Search time 55 Seconds
(without alignments)
46.235 Million cell updates/sec

Title: US-09-734-628-1

Perfect score: 65

Sequence: 1 CDCRGDCFC 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001s:*
5: Geneseq2002s:*
6: Geneseq2003as:*
7: Geneseq2003bs:*
8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	65	100.0	9	2	AAR76200
2	65	100.0	9	2	AAW60289
3	65	100.0	9	2	AAW56034
4	65	100.0	9	2	AAW42255
5	65	100.0	9	2	AAW43233
6	65	100.0	9	2	AAW93626
7	65	100.0	9	2	AAW48821
8	65	100.0	9	3	AAW54271
9	65	100.0	9	3	AAW44970
10	65	100.0	9	3	AAW17928
11	65	100.0	9	3	AAW17964
12	65	100.0	9	3	AAW17346
13	65	100.0	9	3	AAW90211
14	65	100.0	9	3	AAO22875
15	65	100.0	9	3	AAW21701
16	65	100.0	9	4	AAW20271
17	65	100.0	9	4	AAW50242
18	65	100.0	9	4	AAW97086
19	65	100.0	9	4	AAE06279
20	65	100.0	9	4	AAE11044
21	65	100.0	9	5	AAU98837
22	65	100.0	9	5	ABG5079
23	65	100.0	9	5	AAU81110
24	65	100.0	9	5	AAU81134
25	65	100.0	9	5	ABP54051

26	65	100.0	9	5	ABB72945	Integrin
27	65	100.0	9	5	ABB72961	Integrin
28	65	100.0	9	5	ABJ04359	BRASIL me
29	65	100.0	9	5	ABB08066	Cyclic RG
30	65	100.0	9	5	ABG70729	avB3 bind
31	65	100.0	9	5	ABB76442	RGD-4C Pe
32	65	100.0	9	5	AAE17983	Human lig
33	65	100.0	9	5	ABB78354	Amino aci
34	65	100.0	9	5	ABG70754	Targeting
35	65	100.0	9	5	AAU75609	Synthetic
36	65	100.0	9	5	AAU79138	Synthetic
37	65	100.0	9	5	AAU98972	Adeno-ass
38	65	100.0	9	5	AAW48795	Tumour-ta
39	65	100.0	9	5	ABB79525	RGD motif
40	65	100.0	9	5	ABG31063	Alpha v b
41	65	100.0	9	5	AAW78427	Cyclic pe
42	65	100.0	9	5	AAW51995	Drug carg
43	65	100.0	9	6	ABG73024	Integrin
44	65	100.0	9	6	ABB84641	Human int
45	65	100.0	9	6	ABU59556	Tumour an

ALIGNMENTS

RESULT 1

AAR76200
ID AAR76200 standard; peptide; 9 AA.

XX AC AAR76200;

XX DT 24-JAN-1996 (first entry)

XX DE Alphav/beta3 and alphav/beta5 integrin binding peptide #4.

XX KW High affinity; integrin binding peptide; alphas/betal; alphav/beta5;
KW alphav/beta3; RGD; stable configuration; wound healing;
KW osteoclast attachemnt; bone; angiogenesis; metastasis; tumour;
KW smooth muscle cell migration.

XX OS Synthetic.

XX WO9514714-AL.

XX PD 01-JUN-1995.

XX PF 22-NOV-1994; 94WO-US013542.

XX PR 24-NOV-1993; 93US-00158001.

XX PR 04-AUG-1994; 94US-00286861.

XX PA (LJOL-) LA JOLLA CANCER RES FOUND.

XX PI Ruoslahti E, Koivunen E;

XX DR WPI; 1995-206899/27.

XX PT High affinity integrin binding peptides - can be used to attach cells to
PT a substrate, inhibit the attachment of osteoclasts to bone, promote wound
PT healing, inhibit angiogenesis, metastasis of tumours and migration of
PT smooth muscle cells.

XX PS Claim 21; Page 62; 86pp; English.

XX CC The sequences given in AAR76185-200 and AAR79073-94 are high affinity
CC integrin binding peptides which bind to various integrins. Peptides which
CC bind to alphas/beta1 integrins contain the motifs given in AAR76185-86
CC and peptides which bind to alphav/beta5 and alphav/beta3 integrins
CC contain the motif given in AAR76187. Alphav/beta5 integrins are also
CC bound by RGD containing peptides. These peptides assume a
CC conformationally stabilised configuration which is due to the formation
CC of a disulphide bond, a peptide bond or a lactam bond. These peptides may
CC be used for isolating the complementary integrin from a sample mixture by

CC contacting them under ionic conditions to allow binding of the integrin
CC to the peptide and then separating the integrin from the peptide. They
CC can be used for attaching cells to a substrate, by binding them to the
CC substrate with the cell. The peptides promote wound healing when applied
CC locally and inhibit the attachment of osteoclasts to bone. They inhibit
CC angiogenesis, metastasis of tumours and migration of smooth muscle cells
XX
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 65; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDCRGDCFC 9
Db 1 CDCRGDCFC 9

RESULT 2
AAW60289
ID AAW60289 standard; peptide; 9 AA.

XX AC AAW60289;
XX DT 24-AUG-1998 (first entry)

XX DE Tumour homing peptide of the invention.

XX KW Tumour homing peptide; in vivo panning;
XX alpha-V-containing integrin binding motif; tumour.

XX OS Unidentified.
XX PN W09810795-A2.
XX PD 19-MAR-1998.

XX PF 10-SEP-1997; 97WO-US016086.
XX PR 10-SEP-1996; 96US-00710067.

XX PA (BURN-) BURNHAM INST.

XX PI Ruoslahti E, Pasqualini R;

XX DR WPI; 1998-207151/18.

XX PT Tumour homing molecules and their conjugates - useful for, e.g. directing
XX linked moiety to tumour containing angiogenic vasculature.

XX PS Claim 6; Page 91; 105pp; English.

XX CC The present peptide represents a tumour homing peptide, and is produced
XX by in vivo panning. The peptide has an alpha-V-containing integrin
XX binding motif, Arg-Gly-Asp (RGD). The in vivo panning comprises
XX administering a library of diverse peptides to a subject having a tumour,
XX collecting a sample of the tumour, identifying a peptide that homes to
XX the tumour, collecting a sample of normal tissue corresponding to the
XX tumour, and determining that the peptide that homes to the tumour is not
XX present in the normal tissue. The tumour homing peptide can be linked to
XX a moiety (e.g. doxorubicin), and used to direct the moiety to a tumour
XX

SQ Sequence 9 AA;

Query Match 100.0%; Score 65; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDCRGDCFC 9
Db 1 CDCRGDCFC 9

RESULT 3
AAW56034
ID AAW56034 standard; peptide; 9 AA.

XX AC AAW56034;

XX DT 29-JUL-1998 (first entry)

XX DE Chimeric adenovirus fiber protein non-native amino acid sequence 3.

XX KW Chimeric; adenovirus; fiber protein; binding; targeting; coat protein;
XX constrained peptide motif; gene therapy; cancer; heart disease;
XX autoimmune disorder.

XX OS Synthetic.
XX OS Mastadenovirus.

XX PN W09807865-A1.

XX PD 26-FEB-1998.

XX PF 21-AUG-1997; 97WO-US014719.

XX PR 21-AUG-1996; 96US-00701124.

XX PA (GENV-) GENVEC INC.

XX PI Wickham TJ, Roelvink PW, Kovessi I;

XX DR WPI; 1998-169169/15.

XX PT Chimeric adenovirus fibre proteins - containing non-native amino acid
XX sequence to provide for binding and entry into cells, especially for gene
XX therapy.

XX PS Claim 7; Page 68; 124pp; English.

XX CC The present sequence represents a specifically claimed non-native amino
XX acid sequence from a chimeric adenovirus fibre protein (AFP) of the
XX present invention. The non-native amino acid sequence allows the chimeric
XX fibre (or a vector comprising the chimeric fibre) to more efficiently
XX bind to and enter cells. The products can be used for gene therapy, for
XX treating cancer, e.g. melanoma, glioma and lung cancers as well as
XX genetic disorders, e.g. cystic fibrosis, haemophilia and muscular
XX dystrophy as well as pathogenic infections, e.g. HIV, tuberculosis and
XX hepatitis and also for heart disease, to e.g. prevent restenosis
XX following angioplasty or to promote angiogenesis to reperfuse necrotic
XX tissue, and in autoimmune disorders, e.g. Crohn's disease, colitis,
XX rheumatoid arthritis, and Alzheimer's disease
XX

SQ Sequence 9 AA;

Query Match 100.0%; Score 65; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDCRGDCFC 9
Db 1 CDCRGDCFC 9

RESULT 4

AAV42255
ID AAV42255 standard; peptide; 9 AA.

XX AC AAV42255;

XX DT 01-DEC-1999 (first entry)

XX DE Synthetic RGD-4C peptide.

XX KW Adenovirus; gene therapy; coxsackievirus adenovirus receptor; CAR;
XX cancer; cystic fibrosis; muscular dystrophy.

XX OS Synthetic.
 XX PN WO9939734-A1.
 XX XD 12-AUG-1999.
 XX PF 05-FEB-1999; 99WO-US002549.
 XX PR 06-FEB-1999; 98US-0073947P.
 XX PR 10-SEP-1998; 98US-0099801P.
 XX PA (UABR-) UAB RES FOUND.
 XX PI Curriel DT, Krasnykh VN, Dmitriev I;
 XX DR WPI; 1999-539951/45.
 XX PT Recombinant adenovirus vectors with modified fiber knob loops, useful in
 XX gene therapy.
 XX PS Example 21; Page 49; 126pp; English.
 XX CC This sequence represents a synthetic RGD-4C peptide. DNA encoding this
 CC sequence was cloned into the sequence encoding the HI loop of the
 CC adenovirus fibre protein knob domain. This was then used in the
 CC construction of plasmids encoding a modified fibre protein. Recombinant
 CC adenovirus genomes were generated by homologous DNA recombination in E.
 CC coli, before excision of the newly generated genome for virus rescue. The
 CC knob domain of the adenovirus fibre protein mediates the initial binding
 CC and recognition of the coxsackievirus and adenovirus receptor (CAR) on
 CC the cell surface. The HI loop protrudes from the knob domain and connects
 CC beta-strands involved in the formation of the cell binding site.
 CC Recombinant adenovirus vectors are used in a number of gene therapy
 CC applications; however, the reliance on the CAR means that in certain
 CC situations, recombinant viruses are sequestered by high CAR-expressing
 CC non-target cells while the true target cells, if low in CAR, receive
 CC little of the therapeutic gene. Modification of the HI loop by
 CC replacement of the hypervariable region of the loop with a peptide such
 CC as the RGD peptide results in the ability of the virus to utilise an
 CC alternative receptor during the cell entry process. Modifying the
 CC adenovirus fibre knob protein in this way increases the ability of an
 CC adenovirus to transduce a tumour cell in vitro, in vivo and ex vivo. The
 CC vector Ad5HIFLAG incorporating an RGD peptide demonstrated two to three
 CC orders of magnitude of increased gene transfer to ovarian cancer cells.
 CC The modified adenovirus has an altered tropism, which allows the
 CC adenovirus to be targeted to selected cell types. The recombinant
 CC adenovirus can be used to provide gene therapy for individuals suffering
 CC from cancer, cystic fibrosis and Duchenne's muscular dystrophy
 XX SQ Sequence 9 AA;
 Query Match 100.0%; Score 65; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CDCRGDCFC 9
 |||||
 Db 1 CDCRGDCFC 9
 RESULT 5
 AAY43233
 ID AAY43233 standard; peptide; 9 AA.
 XX AC AAY43233;
 XX DT 13-JAN-2000 (first entry)
 XX DE RGD-containing peptide #12.
 XX CC Nucleic acid delivery vehicle; bifunctional complex; transgene; CFTR;
 KW cell surface targeting; cell surface molecule binding region; integrin;

KW cystic fibrosis transmembrane regulator; alphas-antitrypsin;
 KW suicide gene; beta-glucocerebrosidase; cell transfection; cell infection;
 XX RGD peptide.
 OS Synthetic.
 XX PN WO9940214-A2.
 XX PD 12-AUG-1999.
 XX PP 08-FEB-1999; 99WO-US002680.
 XX PR 09-FEB-1998; 98US-00020483.
 XX PR 09-FEB-1998; 98US-0135092P.
 XX PR 06-NOV-1998; 98US-0107471P.
 XX PA (GENZ) GENZYME CORP.
 XX PI O'riordan C, Romanczuk H, Wadsworth SC;
 XX DR WPI; 1999-610583/52.
 XX PT Nucleic acid delivery vehicles useful for transfecting and infecting a
 XX target cell.
 XX PS Claim 22; Page 39; 118pp; English.
 XX CC This sequence represents a RGD-containing peptide that can be used in a
 CC bifunctional complex used in the nucleic acid delivery vehicle (I) of the
 CC invention. (I) is for transfecting and/or infecting a target cell, and
 CC comprises a transgene and a bifunctional complex (B) that targets the
 CC nucleic acid delivery vehicle to the cell surface. (B) comprises a
 CC delivery vehicle binding portion, a cell surface molecule binding portion
 CC (such as this sequence) and a linker connecting them. The delivery
 CC vehicle can be specifically targeted to the cell via the binding to cell
 CC surface molecules. (I) can be used to target cells, which express
 CC integrins such as, Hn-29 colon carcinoma cells, lymphocytes and
 CC osteosarcoma cell line, vascular endothelial cells and melanoma cells.
 CC (I) is useful for delivery of nucleic acids encoding CFTR (cystic
 CC fibrosis transmembrane regulator), alphas-antitrypsin, beta-
 CC glucocerebrosidase and suicide genes. The construct increases the
 CC efficiency of cellular uptake of (I). The constructs also enable the
 CC transfection/infection of cells that are normally refractory to
 CC transfection/infection by targeting cell receptors that are present on
 CC such cells
 XX SQ Sequence 9 AA;
 Query Match 100.0%; Score 65; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CDCRGDCFC 9
 |||||
 Db 1 CDCRGDCFC 9
 RESULT 6
 AAW93626
 ID AAW93626 standard; protein; 9 AA.
 XX AC AAW93626;
 XX DT 28-JUN-1999 (first entry)
 XX DE NGR receptor binding tumour homing peptide 5.
 XX KW Tumour homing peptide; tumour; diagnosis; endothelial cell;
 KW angiogenic vasculature; anti-tumour; anti-inflammatory; anti-angiogenic;
 KW anti-arthritis; NGR receptor; inhibitor; angiogenesis; anticancer drug;
 KW prognosis; inflammation; regeneration; wounded tissue; targeting;
 KW macular degeneration; diabetic retinopathy; rheumatoid arthritis;

occlusive thrombus.
 Synthetic.
 WO9913329-A1.
 18-MAR-1999.
 08-SEP-1998; 98WO-US018895.
 10-SEP-1997; 97US-00926914.
 25-AUG-1998; 98US-00139802.
 (BURN-) BURNHAM INST.
 Ruoslahti E, Pasqualini R;
 WPI; 1999-215158/18.
 Identifying molecules that home to angiogenic vasculature used as targets
 for anticancer agents.
 Claim 15; Page 7; 180pp; English.
 This invention describes novel peptides which home to angiogenic
 vasculature, specifically of a tumour and which have anti-tumour, anti-
 inflammatory, anti-angiogenic and anti-arthritis activity. Such molecules
 are identified by treating a purified NGR receptor with a test compound
 and identifying compounds that bind specifically to the NGR receptor. The
 peptides of the invention are inhibitors of angiogenesis and can be used
 to produce conjugates for delivering agents to angiogenic vasculature,
 particularly anticancer drugs or an imaging agent, for diagnosis or
 prognosis. These conjugates may be directed to non-tumour angiogenic
 vasculature, e.g. that present in inflammatory, regenerating or wounded
 tissue, e.g. for treatment of macular degeneration, diabetic retinopathy
 or rheumatoid arthritis. The peptides provide specific targeting to
 tumours, especially their supporting vasculature, since the NGR receptor
 is exposed to the circulation only in angiogenic vasculature. Precise
 targeting should reduce the systemic toxicity of anticancer drugs in the
 conjugates. Complete killing of all target cells may not be essential
 since partial denudation of endothelium may result in an occlusive
 thrombus, and endothelial cells are unlikely to become resistant to
 anticancer agents nor to lose the targeting receptor. AA93622-W93809 and
 AA93843-44 are examples of tumour homing peptides used in the invention
 Sequence 9 AA;
 Query Match 100.0%; Score 65; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CDCRGDCFC 9
 Db 1 CDCRGDCFC 9
 RESULT 7
 AA48821
 ID AA48821 standard; peptide; 9 AA.
 XX
 AC AA48821;
 XX
 XX 20-MAR-2003 (revised)
 DT 10-DEC-1999 (first entry)
 XX
 DE Membrane dipeptidase-binding retina homing peptide #7.
 XX
 KW Homing peptide; organ; tissue; lung; pancreas; skin; retina; MDP;
 KW prostate; ovary; lymph node; adrenal gland; liver; gut; tumour;
 KW membrane dipeptidase.
 XX
 OS Synthetic.
 OS Homo sapiens.

WO9946284-A2.
 16-SEP-1999.
 10-MAR-1999; 99WO-US005284.
 13-MAR-1998; 98US-00042107.
 26-FEB-1999; 99US-00258754.
 (BURN-) BURNHAM INST.
 Rajotte D, Pasqualini R, Ruoslahti EI;
 WPI; 1999-571717/48.
 New peptides which selectively home to organs or tissues, used for, e.g.
 identifying target ligands and for therapy of pathological conditions.
 Example 6; Page 149; 193pp; English.
 The present invention describes peptides that selectively home to a
 tissue or organ. The peptides can be used for identifying an organ or
 tissue, for identifying a target molecule expressed by an organ or tissue
 or for treating an organ or tissue pathology, where the organ or tissue
 is selected from prostate, lung, skin, retina, pancreas, gut, ovary,
 adrenal gland, liver, and lymph node. The peptide bind to the membrane
 dipeptidase (MDP). AA48618 to AA49066 represent sequences which are
 used in the exemplification of the present invention. (Updated on 20-MAR-
 2003 to correct PR field.)
 XX
 XX Sequence 9 AA;
 Query Match 100.0%; Score 65; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CDCRGDCFC 9
 Db 1 CDCRGDCFC 9
 RESULT 8
 AA54271
 ID AA54271 standard; peptide; 9 AA.
 XX
 AC AA54271;
 XX
 XX 06-APR-2000 (first entry)
 DT
 XX Alpha Vbeta-3 binding peptide sequence.
 DE
 XX Envelope protein; mutant; retrovirus; surface protein shedding;
 KW envelope protein stability; gene therapy; drug therapy; cancer;
 KW adenosine deaminase deficiency; thalassemia; hemophilia; diabetes;
 KW alpha-anti trypsin deficiency; brain disorder; neural disorder;
 KW phenylketonuria; growth disorder; heart disease; immune disease.
 XX
 OS Unidentified.
 XX
 XX WO9960110-A2.
 XX
 XX 25-NOV-1999.
 XX
 XX 20-MAY-1999; 99WO-US011155.
 DP
 XX 20-MAY-1998; 98US-0086149P.
 PR
 XX (UYTE-) UNIV TENNESSEE RES CORP.
 PA Albritton LM, Zavorotinskaya T;
 PI
 XX WPI; 2000-116313/10.
 DR

XX Novel isolated nucleic acid, useful for gene therapy.
 PT
 XX
 PS Example 10; Page 84; 190pp; English.
 XX
 CC The specification describes mutant retrovirus envelope proteins. The
 CC envelope protein coding sequence can be mutated to encode a mutant
 CC envelope protein with a substitution of one or more amino acids in at
 CC least one motif of the retrovirus protein. The mutant protein fragment
 CC allows for decreased shedding of the surface protein by suppressing
 CC precursor cleavage and increase envelope stability and fusion of
 CC retroviruses with cell membranes, while maintaining mutant envelope
 CC protein incorporation into a virion, and viral titers of about two orders
 CC of magnitude within that observed for wild-type retrovirus when the
 CC protein or fragment is expressed on the surface of a retroviral particle.
 CC The proteins have an increased ability to penetrate targets, typically
 CC cells and a correspondingly increased ability to deliver nucleic acids or
 CC drugs. The mutated nucleic acid is useful for gene and drug therapy,
 CC especially as drug delivery vehicles. The retrovirus particles can be
 CC utilized to transduce eukaryotic cells. The transduced cells are useful
 CC in the treatment of cancer in a human. Other diseases contemplated for
 CC treatment include adenosine deaminase deficiency (ADA), thalassemia,
 CC hemophilia, diabetes, alpha-anti trypsin deficiency, brain and neural
 CC disorders, phenylketonuria, growth disorders, heart diseases and immune
 CC diseases. The present sequence was used in the course of the invention,
 CC to quantitate targeted retroviral vector gene delivery in vivo
 XX
 SQ Sequence 9 AA;
 Query Match 100.0%; Score 65; DB 3; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CDCRGDCFC 9
 |||||
 DB 1 CDCRGDCFC 9
 |||||
 RESULT 9
 AAY44970
 ID AAY44970 standard; protein; 9 AA.
 AC AAY44970;
 XX
 DT 23-MAY-2000 (first entry)
 XX
 DE RGD-4C targeting sequence for KDEL receptor inhibitor protein.
 KW KDEL receptor inhibitor; heat shock protein; immune response;
 KW oligomerisation domain; neoplasia; sarcoma; lymphoma; leukaemia;
 KW melanoma; carcinoma; glioblastoma; astrocytoma; oncogene;
 KW infectious disease; allergy; autoimmune disease.
 XX
 OS Unidentified.
 XX
 PN WO200006729-A1.
 PD 10-FEB-2000.
 XX
 PF 28-JUL-1999; 99WO-US017147.
 XX
 PR 29-JUL-1998; 98US-00124671.
 XX
 PA (SLOK) SLOAN KETTERING INST CANCER RES.
 XX
 PI Rothman JF, Mayhew M, Hoe MH;
 XX
 DR WPI; 2000-195296/17.
 XX
 XX Inhibitors of the KDEL receptor which comprises an oligomerization domain
 PT useful for promoting secretion of proteins which are normally retained
 PT within the cell.
 XX

PS Disclosure; Page 17; 87pp; English.
 XX
 CC The patent discloses the use of KDEL receptor inhibitor to promote
 CC secretion of proteins that are normally retained within the cell such as
 CC heat shock proteins by inhibiting KDEL receptor-mediated return of
 CC protein complexes to endoplasmic reticulum. This makes the secreted heat
 CC shock proteins more accessible to the immune system and improves immune
 CC response to a target antigen. The inhibitor protein comprises several
 CC subunits where each subunit comprises an oligomerisation domain and has
 CC at its carboxy terminus a region which binds to a KDEL receptor. The
 CC target antigen may be associated with diseases including neoplasia such
 CC as sarcoma, lymphoma, leukemia, melanoma, carcinoma, glioblastoma and
 CC astrocytoma, with defective tumour suppressor genes, oncogenes,
 CC infectious diseases, allergy or autoimmune diseases. The present sequence
 CC is a targeting peptide termed RGD-4C. This may be incorporated into the
 CC amino terminal region of a KDEL receptor inhibitor protein downstream
 CC from a cleavably removed sequence to improve its activity or alter its
 CC immunogenicity
 XX
 SQ Sequence 9 AA;
 Query Match 100.0%; Score 65; DB 3; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CDCRGDCFC 9
 |||||
 DB 1 CDCRGDCFC 9
 |||||
 RESULT 10
 AAB17928
 ID AAB17928 standard; peptide; 9 AA.
 AC AAB17928;
 XX
 DT 31-OCT-2000 (first entry)
 XX
 DE TPO-mimetic peptide sequence SEQ ID NO:1032.
 KW Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
 KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
 KW immunosuppressive; EPO; TPO; C11A4; mimetic; IL-1; TNF; antagonist; MMP;
 KW inhibitor; erythropoietin; thrombopoietin; interleukin 1;
 KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
 KW vascular endothelial growth factor; matrix metalloproteinase; asthma;
 KW thrombosis; pharmaceutical.
 XX
 OS Synthetic.
 XX
 PN WO2000024782-A2.
 XX
 PD 04-MAY-2000.
 XX
 PF 25-OCT-1999; 99WO-US025044.
 XX
 PR 23-OCT-1998; 98US-0105371P.
 XX
 PR 22-OCT-1999; 99US-00428082.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Feige U, Liu C, Cheetham J, Boone TC;
 XX
 DR WPI; 2000-350702/30.
 XX
 XX Novel composition of matter comprising an Fc domain and pharmacologically
 PT active peptides, useful for treating cancer and autoimmune diseases.
 XX
 PS Disclosure; Page 559; 608pp; English.
 XX
 CC The present invention describes composition of matter (I) comprising an
 CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
 CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each

CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently 0 or 1, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention

XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 65; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDCRGDCFC 9
DB 1 CDCRGDCFC 9

RESULT 11

AAB17964

ID AAB17964 standard; peptide; 9 AA.

AC AAB17964;

XX 31-OCT-2000 (first entry)

DE Integrin-binding peptide sequence SEQ ID NO:1076.

XX Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.

XX Synthetic.

OS WO200024782-A2.

XX 04-MAY-2000.

XX 25-OCT-1999; 99WO-US025044.

XX 23-OCT-1998; 98US-0105371P.

XX 22-OCT-1999; 99US-00428082.

XX (AMGE-) AMGEN INC.

XX Feige U, Liu C, Cheetham J, Boone TC;

XX WPI; 2000-350702/30.

XX Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and autoimmune diseases.

XX Claim 39; Page 591; 608pp; English.

XX The present invention describes composition of matter (I) comprising an Fc domain, pharmacologically active peptides, and linkers. Where (I) is: (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently 0 or 1, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention

CC peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently 0 or 1, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention

XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 65; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDCRGDCFC 9
DB 1 CDCRGDCFC 9

RESULT 12

AAB17346

ID AAB17346 standard; peptide; 9 AA.

AC AAB17346;

XX 31-OCT-2000 (first entry)

DE Integrin-binding peptide sequence SEQ ID NO:450.

XX Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.

XX Synthetic.

OS WO200024782-A2.

XX 04-MAY-2000.

XX 25-OCT-1999; 99WO-US025044.

XX 23-OCT-1998; 98US-0105371P.

XX 22-OCT-1999; 99US-00428082.

XX (AMGE-) AMGEN INC.

XX Feige U, Liu C, Cheetham J, Boone TC;

XX WPI; 2000-350702/30.

XX Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and autoimmune diseases.

XX Claim 39; Page 354; 608pp; English.

XX The present invention describes composition of matter (I) comprising an Fc domain, pharmacologically active peptides, and linkers. Where (I) is: (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently 0 or 1, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic,

CC thrombolytic and immunosuppressive activities. DNAs, vectors and host
 CC cells from the present invention can be used for producing pharmaceutical
 CC compositions. The compositions are useful for treating cancer, asthma,
 CC thrombosis, or autoimmune diseases. The use of an Fc domain (rather than
 CC a Fab domain) can provide a longer half-life or incorporate functions
 CC such as Fc receptor binding, protein A binding, complement fixation, and
 CC possibly placental transfer. AA69443 to AA69526 and AA6955 to
 CC AAB18003 represent nucleotide and amino acid sequences used in the
 CC exemplification of the present invention
 XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 65; DB 3; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDCRGDCFC 9
 |||||
 Db 1 CDCRGDCFC 9

RESULT 13
 AAY90211
 ID AAY90211 standard; peptide; 9 AA.
 XX
 AC AAY90211;
 XX
 DT 06-AUG-2003 (revised)
 DT 21-SEP-2000 (first entry)
 XX
 XX
 DE Alphav integrin targeting peptide #1.
 XX
 KW Ligand epitope; UPAR; urokinase-type plasminogen activator receptor;
 KW adenovirus; hexon HVR5 loop; hexon HI loop; peripheral artery disease;
 KW recombinant adenovirus vector; tumour; restenosis; gene therapy; asthma;
 KW smooth muscle cell proliferation inhibitor; coronary artery disease;
 KW obesity; neurodegenerative disease; infection; autoimmune disease; HIV;
 KW thrombosis; diabetes; tropism-modified virus.
 XX
 OS Synthetic.
 XX
 PN WO200012738-A1.
 XX
 PD 09-MAR-2000.
 XX
 PF 27-AUG-1999; 99WO-IB001524.
 XX
 PR 27-AUG-1998; 98US-0098028P.
 XX
 PA (AVET) AVENTIS PHARMA SA.
 XX
 PI Vigne E, Dedieu J, Latta M, Yeh P, Perricaudet M;
 XX
 DR WPI; 2000-256653/22.
 XX
 XX Urokinase-type plasminogen activator receptor (UPAR)-targeted adenovirus
 PT vectors having modified hexon HVR5 and HI loops and modified fiber
 PT proteins useful for targeted gene therapy to treat cancer or restenosis.
 XX
 PS Example 5; Page 53; 128pp; English.
 XX
 CC This sequence represents a alphav integrin targeting peptide. The
 CC invention relates to an adenovirus from which at least a part of the
 CC hexon HVR5 or HI loop is replaced with a binding peptide, or targeting
 CC sequence, flanked by connecting amino acid spacers, to functionally
 CC display its binding specificity at the capsid surface. The invention also
 CC relates to a recombinant adenovirus vector where a binding peptide, or
 CC targeting sequence, is connected to the C-terminus of the fiber by a
 CC connecting spacer, or linker, so as to functionally display its binding
 CC specificity at the capsid surface. The adenovirus or recombinant
 CC adenovirus vector can be used to preferentially express a gene in a
 CC target cell, especially a cell that expresses a UPAR. The targeted
 CC adenovirus vector preferably comprises a heterologous gene encoding a

CC gene for treatment of a tumour or restenosis. The targeted adenovirus
 CC vector is useful for gene therapy treatment of a disease, and for
 CC manufacturing a medicine used in gene therapy treatment of a disease. The
 CC viruses can also be used to inhibit smooth muscle cell proliferation, to
 CC treat peripheral artery diseases, coronary artery diseases, obesity,
 CC neurodegenerative diseases, infections, autoimmune diseases, asthma, HIV,
 CC thrombosis, and diabetes. The viruses are particularly targeted against a
 CC urokinase-type plasminogen activator receptor (UPAR). The adenoviruses
 CC are tropism-modified without adversely impacting productivity of the
 CC vectors. (Updated on 06-AUG-2003 to correct OS field.)
 XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 65; DB 3; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDCRGDCFC 9
 |||||
 Db 1 CDCRGDCFC 9

RESULT 14
 AAO22875
 ID AAO22875 standard; peptide; 9 AA.
 XX
 AC AAO22875;
 XX
 DT 30-JAN-2003 (first entry)
 DT
 XX
 DE Angiogenic treatment compound related synthetic peptide #75.
 XX
 KW Cyclic; cytostatic; antitumour; targeting moiety; chelator; peptide;
 KW peptidomimetic; angiogenesis; metallopharmaceutical; new blood vessel;
 KW rheumatoid arthritis; cancer; cancer planar; SPECT gamma scintigraphy;
 KW positron emission; X-ray computed tomography; magnetic resonance imaging;
 KW synthetic cyclic peptide.
 XX
 OS Synthetic.
 XX
 PN WO958162-A2.
 XX
 PD 18-NOV-1999.
 XX
 PF 29-MAR-1999; 99WO-US006826.
 XX
 PR 31-MAR-1998; 98US-0080150P.
 PR 18-DEC-1998; 98US-0112715P.
 XX
 PA (DUPO) DU PONT PHARM CO.
 XX
 PI Rajopadhye M, Edwards DS, Harris TD, Heminway SJ, Liu S;
 PI Singh PR;
 XX
 DR WPI; 2000-105546/09.
 XX
 PT Novel compound for diagnosis and treatment of cancer.
 XX
 PS Disclosure; Page 62; 213pp; English.
 XX
 CC The invention relates to compounds comprising targeting moiety which is
 CC bound to a chelator. The targeting moiety is a peptide or peptidomimetic
 CC which binds to a receptor and is upregulated during angiogenesis. The
 CC compound has 0-1 linking groups between targeting moiety and the
 CC chelator. The metallopharmaceutical composition is used in treating
 CC rheumatoid arthritis or cancer by imaging the formation of new blood
 CC vessels, imaging cancer planar or SPECT gamma scintigraphy, positron
 CC emission or X-ray computed tomography or with magnetic resonance imaging.
 CC This sequence represents a synthetic cyclic peptide relating to the novel
 CC compounds of the invention
 XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 65; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDCRGDCFC 9
| | | | |
Db 1 CDCRGDCFC 9

RESULT 15

AAB21701
ID AAB21701 standard; peptide; 9 AA.

XX
AC AAB21701;

XX
DT 22-MAR-2001 (first entry)

XX
XX Human breast tumour homing peptide #1.

XX
KW Cytostatic; homing pro-apoptotic conjugate; tumour; antimicrobial;
KW breast; prostate; melanoma; cancer; Kaposi's sarcoma; human.

XX
OS Homo sapiens.

XX
PN WO200042973-A2.

XX
XX 27-JUL-2000.

XX
PF 21-JAN-2000; 2000WO-US001602.

XX
PR 22-JAN-1999; 99US-00235902.

XX
XX (BURN-) BURNHAM INST.

XX
PI Ellerby HM, Bredesen DE, Pasqualini R, Ruoslahti EI;

XX
DR WPI; 2000-499174/44.

XX
PT Homing pro-apoptotic conjugate comprising a tumor homing molecule that
PT selectively homes to a mammalian cell type or tissue linked to an
PT antimicrobial peptide, useful for the treatment of prostate cancer.

XX
PS Claim 12; Page 105; 118pp; English.

XX
CC The present invention relates to homing pro-apoptotic conjugates,
CC comprising of a tumour homing molecule that selectively homes to a
CC mammalian cell type or tissue, linked to an antimicrobial peptide. The
CC homing pro-apoptotic conjugates are selectively internalised by the
CC mammalian cell type or tissue and exhibits high toxicity, especially to
CC angiogenic vasculature. The antimicrobial peptide has low mammalian cell
CC toxicity when not linked to the tumor homing molecule. The conjugates are
CC useful for the treatment of cancer e.g. Kaposi's sarcoma, breast and
CC prostate cancer or melanoma. The present sequence is a homing peptide
CC isolated in the present invention, which can be conjugated to an
CC antimicrobial peptide to make the homing pro-apoptotic conjugates of the
CC present invention

SQ Sequence 9 AA;

Query Match 100.0%; Score 65; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDCRGDCFC 9
| | | | |
Db 1 CDCRGDCFC 9

Search completed: July 11, 2004, 09:16:06
Job time : 58 secs

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OM protein - protein search, using sw model

Run on: July 11, 2004, 09:16:11 ; Search time 47 Seconds
(without alignments)
59.729 Million cell updates/sec

Title: US-09-734-628-1

Perfect score: 65

Sequence: 1 CDCRGDCFC 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1279676 seqs, 311918243 residues

Total number of hits satisfying chosen parameters: 1279676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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2: /cgn2_6/ptodata/1/pubaa/PTCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubaa/US07_NEW_PUB.pep.*
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7: /cgn2_6/ptodata/1/pubaa/US08_NEW_PUB.pep.*
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11: /cgn2_6/ptodata/1/pubaa/US09C_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	65	100.0	9	US-09-765-086-1	Sequence 1, Appli
2	65	100.0	9	US-09-845-160-5	Sequence 5, Appli
3	65	100.0	9	US-09-245-603A-16	Sequence 16, Appl
4	65	100.0	9	US-09-364-597A-16	Sequence 16, Appl
5	65	100.0	9	US-09-734-628-1	Sequence 1, Appli
6	65	100.0	9	US-09-971-798-5	Sequence 3, Appli
7	65	100.0	9	US-09-969-192-3	Sequence 38, Appl
8	65	100.0	9	US-09-840-277-38	Sequence 62, Appl
9	65	100.0	9	US-09-840-277-62	Sequence 2, Appli
10	65	100.0	9	US-09-801-485-2	Sequence 124, App
11	65	100.0	9	US-09-791-524-124	Sequence 450, App
12	65	100.0	9	US-10-609-217-450	Sequence 1076, Ap
13	65	100.0	9	US-10-609-217-1076	Sequence 166, App
14	65	100.0	9	US-10-363-208-166	Sequence 450, App
15	65	100.0	9	US-10-632-388-1076	

16	65	100.0	9	12	US-10-632-388-1076	Sequence 1076, Ap
17	65	100.0	9	12	US-10-652-244-20	Sequence 20, Appl
18	65	100.0	9	12	US-10-651-723-450	Sequence 450, App
19	65	100.0	9	12	US-10-651-723-1076	Sequence 1076, Ap
20	65	100.0	9	12	US-09-912-609-31	Sequence 31, Appl
21	65	100.0	9	12	US-09-995-388-47	Sequence 47, Appl
22	65	100.0	9	12	US-10-013-009-1	Sequence 1, Appli
23	65	100.0	9	12	US-10-033-789-10	Sequence 10, Appl
24	65	100.0	9	12	US-10-269-575-1	Sequence 1, Appli
25	65	100.0	9	12	US-10-645-761-450	Sequence 450, App
26	65	100.0	9	12	US-10-645-761-1076	Sequence 1076, Ap
27	65	100.0	9	13	US-10-080-854-8	Sequence 8, Appli
28	65	100.0	9	13	US-10-038-972A-10	Sequence 10, Appl
29	65	100.0	9	14	US-10-304-160-3	Sequence 3, Appli
30	65	100.0	9	14	US-10-264-374-1	Sequence 1, Appli
31	65	100.0	9	14	US-10-032-221B-35	Sequence 35, Appl
32	65	100.0	9	14	US-10-375-992-1	Sequence 1, Appli
33	65	100.0	9	16	US-10-666-696-450	Sequence 450, App
34	65	100.0	9	16	US-10-666-696-1076	Sequence 1076, Ap
35	65	100.0	9	16	US-10-653-048-450	Sequence 450, App
36	65	100.0	9	16	US-10-653-048-1076	Sequence 1076, Ap
37	65	100.0	9	16	US-10-264-374-1	Sequence 1, Appl
38	65	100.0	10	9	US-09-845-160-14	Sequence 14, Appl
39	65	100.0	10	9	US-09-870-203A-43	Sequence 43, Appl
40	65	100.0	10	12	US-09-780-142-2	Sequence 2, Appli
41	65	100.0	10	14	US-10-429-496-2	Sequence 2, Appli
42	65	100.0	10	14	US-10-429-428-2	Sequence 2, Appli
43	65	100.0	10	15	US-10-403-337-30	Sequence 30, Appl
44	65	100.0	10	15	US-10-351-830-30	Sequence 30, Appl
45	65	100.0	10	15	US-10-296-879-29	Sequence 29, Appl

ALIGNMENTS

RESULT 1
US-09-765-086-1
; Sequence 1, Application US/09765086
; Patent No. US20010046498A1
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; APPLICANT: Wadih, Arap
; APPLICANT: Bredesen, Dale E.
; APPLICANT: Ellerby, H. Michael
; TITLE OF INVENTION: Chimeric Prostate-Homing Peptides With
; FILE REFERENCE: P-LJ 3844
; CURRENT APPLICATION NUMBER: US/09/765,086
; CURRENT FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US 09/489,582
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 235
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-09-765-086-1

Query Match 100.0%; Score 65; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDCRGDCFC 9

Db 1 CDCRGDCFC 9

RESULT 2

US-09-845-160-5

; Sequence 5, Application US/09845160
; Patent No. US2002058045A1
; GENERAL INFORMATION:
; APPLICANT: MIZUGUCHI, HIROYUKI
; APPLICANT: HAYAKAWA, TAKAO
; TITLE OF INVENTION: ADENOVIRUS VECTOR
; FILE REFERENCE: 081356/0163
; CURRENT APPLICATION NUMBER: US/09/845,160
; CURRENT FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: JP 2001-131688
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: JP 2000-161577
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: RGD-4C peptide.
US-09-845-160-5

Query Match 100.0%; Score 65; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDCRGDCFC 9
Db 1 CDCRGDCFC 9

RESULT 3
US-09-245-603A-16
; Sequence 16, Application US/09245603A
; Patent No. US20020081280A1
; GENERAL INFORMATION:
; APPLICANT: Curiel, David T.
; APPLICANT: Krasnykh, Victor N.
; APPLICANT: Dmitriev, Igor
; TITLE OF INVENTION: Adenovirus Vector Containing A Heterologous Peptide
; FILE REFERENCE: D6080
; CURRENT APPLICATION NUMBER: US/09/245,603A
; CURRENT FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: US 60/099,801
; PRIOR FILING DATE: 1998-09-10
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 16
; LENGTH: 9
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of a RGD peptide incorporated
; OTHER INFORMATION: into the region of the fiber gene within the HI loop.
US-09-245-603A-16

Query Match 100.0%; Score 65; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDCRGDCFC 9
Db 1 CDCRGDCFC 9

RESULT 4
US-09-364-597A-16
; Sequence 16, Application US/09364597A
; Patent No. US20020103130A1
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Koivunen, Erkki

; TITLE OF INVENTION: No. US20020103130A1el Integrin-Binding Peptides
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/364,597A
; FILING DATE: 30-JUL-1999
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/158,001
; FILING DATE: 24-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/286,861
; FILING DATE: 04-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LA 3419
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (858) 535-9001
; TELEFAX: (858) 535-8949
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: circular
US-09-364-597A-16

Query Match 100.0%; Score 65; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDCRGDCFC 9
Db 1 CDCRGDCFC 9

RESULT 5
US-09-734-628-1
; Sequence 1, Application US/09734628
; Patent No. US20020122806A1
; GENERAL INFORMATION:
; APPLICANT: Chinnaiyan, Arul M.
; APPLICANT: Rehmetulla, Alnawaz
; APPLICANT: Ross, Brian D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IN SITU AND
; TITLE OF INVENTION: IN VIVO IMAGING OF CELLS AND TISSUES
; FILE REFERENCE: 11203-005001
; CURRENT APPLICATION NUMBER: US/09/734,628
; CURRENT FILING DATE: 2000-12-11
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-09-734-628-1

Query Match 100.0%; Score 65; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDCRGDCFC 9
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Db 1 CDCRGDCFC 9

RESULT 6

US-09-971-798-5
; Sequence 5, Application US/09971798
; Patent No. US20020132769A1
; GENERAL INFORMATION:
; APPLICANT: NO. US20020132769A1artis AG
; TITLE OF INVENTION: Targeting molecules
; FILE REFERENCE: 4-31615/GTI
; CURRENT APPLICATION NUMBER: US/09/971,798
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-971-798-5

Query Match 100.0%; Score 65; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDCRGDCFC 9
|||||
Db 1 CDCRGDCFC 9

RESULT 7

US-09-969-192-3
; Sequence 3, Application US/09969192
; Patent No. US20020151027A1
; GENERAL INFORMATION:
; APPLICANT: WICKHAM, THOMAS J.
; ROELVINK, PETRUS W.
; KOVESDI, IMRE
; TITLE OF INVENTION: TARGETING ADENOVIRUS WITH USE OF
; CONSTRAINED PEPTIDE MOTIFS
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Voit & Mayer, Ltd.
; STREET: Two Prudential Plaza - 49th Floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/09/969,192
; APPLICATION NUMBER: US/09/969,192
; FILING DATE: 01-Oct-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 9-455061
; FILING DATE: 06-DEC-1999
; APPLICATION NUMBER: US 9-130225
; FILING DATE: 06-AUG-1998
; APPLICATION NUMBER: US 8-701124
; FILING DATE: 21-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hefner, M. Daniel
; REGISTRATION NUMBER: 41,826
; REFERENCE/DOCKET NUMBER: 213564
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids

; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-969-192-3

Query Match 100.0%; Score 65; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDCRGDCFC 9
|||||
Db 1 CDCRGDCFC 9

RESULT 8

US-09-840-277-38
; Sequence 38, Application US/09840277
; Patent No. US20020168363A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: KOHNO, TADAHIKO
; APPLICANT: LACEY, DAVID LEE
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: INTEGRIN/ADHESION ANTAGONISTS
; FILE REFERENCE: A-688A
; CURRENT APPLICATION NUMBER: US/09/840,277
; CURRENT FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: 60/198,919
; PRIOR FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 60/201,394
; PRIOR FILING DATE: 2000-05-03
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Integrin antagonist peptide
US-09-840-277-38

Query Match 100.0%; Score 65; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDCRGDCFC 9
|||||
Db 1 CDCRGDCFC 9

RESULT 9

US-09-840-277-62
; Sequence 62, Application US/09840277
; Patent No. US20020168363A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: KOHNO, TADAHIKO
; APPLICANT: LACEY, DAVID LEE
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: INTEGRIN/ADHESION ANTAGONISTS
; FILE REFERENCE: A-688A
; CURRENT APPLICATION NUMBER: US/09/840,277
; CURRENT FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: 60/198,919
; PRIOR FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 60/201,394
; PRIOR FILING DATE: 2000-05-03
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 62
; LENGTH: 9

```

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Integrin antagonist peptide
US-09-840-277-62

Query Match          100.0%; Score 65; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

Qy 1 CDCRGDCFC 9
Db 1 CDCRGDCFC 9

RESULT 10
US-09-801-485-2
; Sequence 2, Application US/09801485
; Publication No. US20030077819A1
; GENERAL INFORMATION:
; APPLICANT: Dickerson, Erin B
; APPLICANT: Helfand, Stuart C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TARGETING INTERLEUKIN-12
; FILE REFERENCE: WARP-0003
; CURRENT APPLICATION NUMBER: US/09/801,485
; CURRENT FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-801-485-2

Query Match          100.0%; Score 65; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

Qy 1 CDCRGDCFC 9
Db 1 CDCRGDCFC 9

RESULT 11
US-09-791-524-124
; Sequence 124, Application US/09791524
; Publication No. US20030143209A1
; GENERAL INFORMATION:
; APPLICANT: Aventis Pharmaceuticals Products Inc.
; TITLE OF INVENTION: Targeted Adenovirus Vectors For Delivery Of Heterologous Genes
; FILE REFERENCE: A3319A
; CURRENT APPLICATION NUMBER: US/09/791,524
; CURRENT FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/09828
; PRIOR FILING DATE: 1998-08-27
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 124
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Adenovirus
US-09-791-524-124

Query Match          100.0%; Score 65; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

Qy 1 CDCRGDCFC 9
Db 1 CDCRGDCFC 9

```

```

RESULT 12
US-10-609-217-450
; Sequence 450, Application US/10609217
; Publication No. US20040044188A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/609,217
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 450
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: INTEGRIN-BINDING PEPTIDE
US-10-609-217-450

Query Match          100.0%; Score 65; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

Qy 1 CDCRGDCFC 9
Db 1 CDCRGDCFC 9

RESULT 13
US-10-609-217-1076
; Sequence 1076, Application US/10609217
; Publication No. US20040044188A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/609,217
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1076
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: INTEGRIN-BINDING PEPTIDE
US-10-609-217-1076

Query Match          100.0%; Score 65; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

Qy 1 CDCRGDCFC 9
Db 1 CDCRGDCFC 9

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RESULT 14
US-10-363-208-166
; Sequence 166, Application US/10363208
; Publication No. US20040048243A1
; GENERAL INFORMATION:
; APPLICANT: Board of Regents, The University of Texas System
; TITLE OF INVENTION: Methods and Compositions for In Vitro Targeting
; FILE REFERENCE: 005774.P005PCT
; CURRENT APPLICATION NUMBER: US/10/363,208
; CURRENT FILING DATE: 2003-03-07
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 166
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; NAME/KEY: Peptide
; LOCATION: (1)..(9)
; OTHER INFORMATION: synthetic construct
US-10-363-208-166

Query Match 100.0%; Score 65; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CDCRGDCFC 9
Db 1 CDCRGDCFC 9

RESULT 15
US-10-632-388-450
; Sequence 450, Application US/10632388
; Publication No. US20040053845A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/632,388
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 450
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; NAME/KEY: Peptide
; LOCATION: (1)..(9)
; OTHER INFORMATION: INTEGRIN-BINDING PEPTIDE
US-10-632-388-450

Query Match 100.0%; Score 65; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CDCRGDCFC 9
Db 1 CDCRGDCFC 9

Search completed: July 11, 2004, 09:21:50
Job time : 48 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 11, 2004, 09:17:42 ; Search time 11 Seconds
(without alignments)
42.603 Million cell updates/sec

Title: US-09-734-628-1
Perfect score: 65
Sequence: 1 CDCRGDCFC 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 251

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Presd. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	32.3	9	1 COW CONVE	P83047 conus ventr
2	16	24.6	7	1 BRHP_CONIM	P58803 conus imper
3	15	23.1	7	1 FARI_HELTI	P41871 helisoma tr
4	15	23.1	8	1 ACT_CARVA	P80709 carcinus ma
5	15	23.1	9	1 CCAP_CARVA	P38556 carcinus ma
6	15	23.1	9	1 CONO_CONGE	P05486 conus geogr
7	15	23.1	9	1 OXYT_EISFO	P42998 eisenia foe
8	15	23.1	9	1 SAP_STOVA	P24047 stomopneute
9	13	20.0	9	1 DSIP_RABIT	P01158 oryctolagus
10	13	20.0	9	1 TALI_PICJA	P17440 pichia jadi
11	12	18.5	4	1 OCPI_OCTMI	P58648 octopus min
12	12	18.5	5	1 UKA4_CHLTR	P38005 chlamydia t
13	12	18.5	7	1 PPH2_LYCES	P83379 lycopersico
14	12	18.5	8	1 ACI_THUAL	P18691 thunus alb
15	12	18.5	8	1 FARI_PENMO	P83316 penaeus mon
16	12	18.5	8	1 LMT2_LOCFI	P22396 locusta mig
17	12	18.5	8	1 ORMY_ORCLI	P82455 orconectes
18	12	18.5	9	1 ISOT_CYPCL	P42993 cyprinus ca
19	12	18.5	9	1 OXYA_SCYCA	P42996 scyllorhina
20	12	18.5	9	1 OXYA_SQUAC	P42999 squaleus aca
21	12	18.5	9	1 OXYE_SCYCA	P42997 scyllorhina
22	12	18.5	9	1 OXYT_BUFR	P42995 bufo regula
23	12	18.5	9	1 OXYT_CYPCL	P23679 cyprinus ca
24	12	18.5	9	1 OXYT_OCTVU	P80027 octopus vul
25	12	18.5	9	1 OXYT_RABIT	P82878 oryctolagus
26	12	18.5	9	1 OXYT_RAJCL	P42994 raja clavet
27	12	18.5	9	1 OXYV_SQUAC	P43000 squaleus aca
28	12	18.5	9	1 PPH1_LYCES	P83380 lycopersico
29	12	18.5	9	1 UPF6_HUMAN	P30092 homo sapien
30	11	16.9	6	1 FARP_MONEX	P41966 moniezia ex
31	11	16.9	7	1 UF04_MOUSE	P38642 mus musculu
32	11	16.9	8	1 ALL5_CVDPO	P82156 cydia pomon
33	11	16.9	8	1 GLUS_HUMAN	P02729 homo sapien

34	11	16.9	9	1 CONO CONST	P05487 conus stria
35	11	16.9	9	1 DNEI_LOCFI	P16339 locusta mig
36	11	16.9	9	1 FIBE_PAPAN	P19344 papio anubi
37	11	16.9	9	1 PGLR_DIAAS	P81179 diaprepes a
38	11	16.9	9	1 ULAH_HUMAN	P31934 homo sapien
39	10	15.4	5	1 RE11_LITRU	P82070 litoria rub
40	10	15.4	8	1 COW2_CONPU	P58785 conus purpu
41	10	15.4	8	1 RS1_ERWCH	P37985 erwinia chr
42	10	15.4	9	1 TALI_PICJA	P17441 pichia jadi
43	9	13.8	7	1 FARP_CALVO	P41868 calliphora
44	9	13.8	8	1 CCRN_MACEU	P30369 macropus eu
45	9	13.8	8	1 LCKS_LEUMA	P19987 leucophaea

ALIGNMENTS

RESULT 1
COW_CONVE STANDARD; PRT; 9 AA.
AC P83047;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Contryphan-Vn.
OS Conus ventricosus (Mediterranean cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=117992;
RN [1]
RP SEQUENCE, SYNTHESIS, DISULFIDE BONDS, AND MASS SPECTROMETRY.
RC TISSUE=Venom;
RX MEDLINE=21547795; PubMed=11688995;
RA Massilia G.R., Schinina M.E., Ascenzi P., Politicelli F.;
RT "Contryphan-Vn: a novel peptide from the venom of the Mediterranean
snail Conus ventricosus";
RL Biochem. Biophys. Res. Commun. 288:908-913(2001).
RN [2]
RP STRUCTURE BY NMR, SYNTHESIS, DISULFIDE BONDS, AND FUNCTION.
RX MEDLINE=22533239; PubMed=12646193;
RA Massilia G.R., Eliseo T., Grolleau F., Lapiet B., Barbier J.,
RA Bournaud R., Molgo J., Cicero D.O., Paci M., Schinina M.E.,
RA Ascenzi P., Politicelli F.;
RT "Contryphan-Vn: a modulator of Ca2+-dependent K+ channels.";
RL Biochem. Biophys. Res. Commun. 303:238-246(2003).
CC -!- FUNCTION: Affects both voltage-gated and calcium-dependent
potassium channel activities, with composite and diversified
effects in invertebrate and vertebrate systems.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -!- PTM: The cis isomer is the most abundant and is thus thought to be
the functionally relevant conformer.
CC -!- MASS SPECTROMETRY: MW=1088.6; METHOD=MALDI.
CC -!- SIMILARITY: Belongs to the contryphan family.
DR PDB; 1NXX; 04-MAR-03.
KW Toxin; Ionic channel inhibitor; Neurotoxin;
KW Potassium channel inhibitor; D-amino acid; Amidation; 3D-structure.
FT DISULFID 3 9
FT MOD_RES 5 5 D-TRYPTOPHAN.
FT MOD_RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 1091 MW; 8D38676323676EBA CRC64;

Query Match 32.3%; Score 21; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GDC 7
Db 1 GDC 3

RESULT 2

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BRHP CONIM          STANDARD;          PRT;          7 AA.
ID  PS8803;
DT  28-FEB-2003 (Rel. 41, Created)
DT  28-FEB-2003 (Rel. 41, Last sequence update)
DT  28-FEB-2003 (Rel. 41, Last annotation update)
DE  Bromoheptapeptide Im.
OS  Conus imperialis (Imperial cone).
OC  Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC  Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC  Neogastropoda; Conoidea; Conidae; Conus.
OX  NCBI_TaxID=35631;
RN  [1]
RC  SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
RP  TISSUE=Venom;
RA  MEDLINE=97184108; PubMed=9030520;
RA  Craig A.G., Jimenez E.C., Dykert J., Nielsen D.B., Gulyas J.,
RA  Abogadie F.C., Porter J., Rivier J.E., Cruz L.J., Olivera B.M.,
RA  McIntosh J.M.;
RT  "A novel post-translational modification involving bromination of
RT  tryptophan. Identification of the residue, L-6-bromotryptophan, in
RT  peptides from Conus imperialis and Conus radiatus venom.";
RL  J. Biol. Chem. 272:4689-4698(1997).
RC  -1- FUNCTION: Does not elicit gross behavioral symptoms when injected
CC  centrally or peripherally in mice.
CC  -1- SUBCELLULAR LOCATION: Secreted.
CC  -1- TISSUE SPECIFICITY: Expressed by the venom duct.
CC  -1- MASS SPECTROMETRY: MW=853.19; METHOD=LSIMS.
DR  PIR; A58512; A58512.
KW  Bromination; Amidation; Pyrrolidone carboxylic acid.
FT  DISULFID 2 7
FT  MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT  MOD RES 6 6 BROMINATION.
FT  MOD RES 7 7 AMIDATION.
SQ  SEQUENCE 7 AA; 795 MW; 6EA37DC6D87EA680 CRC64;

Query Match 24.6%; Score 16; DB 1; Length 7;
Best Local Similarity 40.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 GDCFC 9
DB 3 GQAWC 7

RESULT 3
FARI HELTI          STANDARD;          PRT;          7 AA.
ID  P41871;
DT  01-NOV-1995 (Rel. 32, Created)
DT  01-NOV-1995 (Rel. 32, Last sequence update)
DT  01-NOV-1995 (Rel. 32, Last annotation update)
DE  FMRamide-like neuropeptide GDFFLRP-amide.
OS  Helisoma trivolvis (Snail).
OC  Eukaryota; Metazoa; Mollusca; Gastropoda; Basommatophora;
OC  Lymnaeidae; Planorbidae; Helisoma.
OX  NCBI_TaxID=27815;
RN  [1]
RC  SEQUENCE
RP  TISSUE=Kidney;
RA  MEDLINE=94286417; PubMed=7912428;
RA  Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;
RT  "FMRamide-related peptides from the kidney of the snail, Helisoma
RT  trivolvis";
RL  Peptides 15:31-36(1994).
CC  -1- FUNCTION: Appears to be involved in osmoregulation by affecting
CC  the kidney mantle and skin.
CC  -1- TISSUE SPECIFICITY: Kidney, skin, mantle and the hemolymph.
CC  -1- SIMILARITY: Belongs to the FARP (FMRamide related peptide)
CC  family.
KW  Neuropeptide; Amidation.
FT  MOD RES 7 7 AMIDATION.
SQ  SEQUENCE 7 AA; 851 MW; 69D40729D76AA810 CRC64;

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Query Match 23.1%; Score 15; DB 1; Length 7;
Best Local Similarity 75.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GDCFC 8
DB 1 GDFP 4

RESULT 4
ACT_CARMA          STANDARD;          PRT;          8 AA.
ID  P80709;
DT  01-OCT-1996 (Rel. 34, Created)
DT  01-OCT-1996 (Rel. 34, Last sequence update)
DT  15-JUL-1999 (Rel. 38, Last annotation update)
DE  Actin (Fragment).
OS  Carcinus maenas (Common shore crab) (Green crab).
OC  Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC  Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC  Eubranchyura; Fortuonoidea; Fortunidae; Carcinus.
OX  NCBI_TaxID=6759;
RN  [1]
RC  SEQUENCE.
RP  Lachaise F., Somme G., Carpentier G., Granjeon E., Webster S.,
RA  Baghdasarian D.; An enzyme implicated in crab steroidogenesis.";
RL  Endocrine 5:23-32(1996).
CC  -1- FUNCTION: Actins are highly conserved proteins that are involved
CC  in various types of cell motility and are ubiquitously expressed
CC  in all eukaryotic cells.
CC  -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC  -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN IS:
CC  6.8. ITS MW IS: 46 kDa.
CC  -1- SIMILARITY: Belongs to the actin family.
DR  InterPro; IPR004001; Actin..
DR  PROSITE; PS004000; ACTIN..
DR  PROSITE; PS00432; ACTINS 1; PARTIAL.
DR  PROSITE; PS00432; ACTINS 2; PARTIAL.
KW  Structural protein.
FT  NON_TER 1 1
FT  NON_TER 8 8
SQ  SEQUENCE 8 AA; 976 MW; 1424005AB2CAAE83 CRC64;

Query Match 23.1%; Score 15; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CD 2
DB 2 CD 3

RESULT 5
CCAP_CARMA          STANDARD;          PRT;          9 AA.
ID  P38556;
DT  01-OCT-1994 (Rel. 30, Created)
DT  01-OCT-1994 (Rel. 30, Last sequence update)
DT  15-MAR-2004 (Rel. 43, Last annotation update)
DE  Cardioactive peptide (CCAP).
OS  Carcinus maenas (Common shore crab) (Green crab),
OS  Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm),
OS  Tenbrio molitor (Yellow mealworm), and
OS  Spodoptera eridania (Southern armyworm).
OC  Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC  Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC  Eubranchyura; Fortuonoidea; Fortunidae; Carcinus.
OX  NCBI_TaxID=6759, 7130, 7067, 37547;
RN  [1]
RC  SEQUENCE.

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RC SPECIES=C.maenas; TISSUE=Pericardial organs;
 RA Stangier J., Hilbich C., Beyreuther K., Keller R.;
 RT "Unusual cardioactive peptide (CCAP) from pericardial organs of the
 RT shore crab Carcinus maenas.";
 RN Proc. Natl. Acad. Sci. U.S.A. 84:575-579(1987).
 RN [2]
 RN SEQUENCE.
 RP SPECIES=M.sexata;
 RC MEDLINE=93050243; PubMed=1426284;
 RX Cheung C.C., Loi P.K., Sylwester A.W., Lee T.D., Tublitz N.J.;
 RA "Primary structure of a cardioactive neuropeptide from the tobacco
 RT hawkmoth, Manduca sexta.";
 RL FEBS Lett. 313:165-168(1992).
 RN [3]
 RN SEQUENCE.
 RP SPECIES=T.molitor, and S.eridania; TISSUE=Head;
 RC MEDLINE=94176032; PubMed=8129851;
 RX Furuya K., Liao S., Reynolds S.B., Ota R.B., Hackett M.,
 RA Schooley D.A.;
 RT "Isolation and identification of a cardioactive peptide from Tenebrio
 RT molitor and Spodoptera eridania.";
 RL Biol. Chem. Hoppe-Seyler 374:1065-1074(1993).
 CC -|- FUNCTION: The effect of CCAP is both ino- and chronotropic.
 CC -|- SUBCELLULAR LOCATION: Secreted.
 CC -|- TISSUE SPECIFICITY: Stored in pericardial organs and released
 CC into the hemolymph.
 DR PIR; A26363; A26363.
 DR PIR; S27233; S27233.
 KW Neuropeptide; Amidation.
 FT DISULFID 3 9
 FT MOD RES 9 9
 SQ SEQUENCE 9 AA; 959 MW; C5A861A9CDD44EB9 CRC64;

Query Match 23.1%; Score 15; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05; Indels 0; Gaps 0;
 Matches 2; Conservative 0; Mismatches 0;

QY 8 FC 9
 ||
 Db 2 FC 3

RESULT 6
 CONO_CONGE STANDARD; PRT; 9 AA.
 AC P05486;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Lys-conopressin G (Geography cone).
 OS Conus geographus (Geography cone).
 CC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
 CC Apgastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
 CC Neogastropoda; Conoidea; Conidae; Conus.
 CC NCBI_TaxID=6491;
 RN [1]
 RN SEQUENCE.
 RP MEDLINE=88058932; PubMed=3680228;
 RX Cruz L.J., de Santos V., Zafaralla G.C., Ramilo C.A., Zeikus R.D.,
 RA Gray W.R., Olivera B.M.;
 RT "Invertebrate vasopressin/oxytocin homologs. Characterization of
 RT peptides from Conus geographus and Conus straitus venoms.";
 RL J. Biol. Chem. 262:15821-15824(1987).
 RN [2]
 RN REVIEW
 RX MEDLINE=89024586; PubMed=3052286;
 RA Gray W.R., Olivera B.M., Cruz L.J.;
 RT "Peptide toxins from venomous Conus snails";
 RL Annu. Rev. Biochem. 57:665-700(1988).
 CC -|- SUBCELLULAR LOCATION: Secreted.
 CC -|- SIMILARITY: Belongs to the vasopressin/oxytocin family.
 DR PIR; A28495; A28495.
 DR InterPro; IPR000981; Neurhyp_horm.

DR Pfam; PF00220; hormone4; 1.
 DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
 KW Hormone; Amidation.
 FT DISULFID 1 6
 FT MOD RES 9 9
 SQ SEQUENCE 9 AA; 1037 MW; D4FC276EB4540059 CRC64;
 Query Match 23.1%; Score 15; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05; Indels 0; Gaps 0;
 Matches 2; Conservative 0; Mismatches 0;

QY 7 CF 8
 ||
 Db 1 CF 2

RESULT 7
 OXYT_EISFO STANDARD; PRT; 9 AA.
 AC P42998;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Anetocin.
 OS Eisenia foetida (Common branding worm) (Common dung-worm).
 CC Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
 CC Lumbricina; Lumbricidae; Eisenia.
 CC NCBI_TaxID=6396;
 RN [1]
 RN SEQUENCE.
 RP TISSUE=Pituitary;
 RC MEDLINE=94121660; PubMed=8292046;
 RX Omi T., Ukena K., Matsushima O., Ikeda T., Fujita T., Minakata H.,
 RA Nomoto K.;
 RT "Anetocin: an oxytocin-related peptide isolated from the earthworm,
 RT Eisenia foetida.";
 RL Biochem. Biophys. Res. Commun. 198:393-399(1994).
 CC -|- FUNCTION: POTENTIATES SPONTANEOUS CONTRACTIONS OF THE GUT AND ALSO
 CC PULSATORY CONTRACTIONS AND BLADDER-SHAKING MOVEMENT OF THE
 CC NEPHRIDIA. MAY BE INVOLVED IN OSMOREGULATION OF THE ANIMAL THROUGH
 CC NEPHRIDIAL FUNCTION.
 CC -|- SIMILARITY: Belongs to the vasopressin/oxytocin family.
 DR PIR; PC2021; PC2021.
 DR InterPro; IPR000981; Neurhyp_horm.
 DR Pfam; PF00220; hormone4; 1.
 DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; FALSE_NEG.
 KW Hormone; Amidation.
 FT DISULFID 1 6
 FT MOD RES 9 9
 SQ SEQUENCE 9 AA; 996 MW; D4EB76EB45412C9 CRC64;

Query Match 23.1%; Score 15; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05; Indels 0; Gaps 0;
 Matches 2; Conservative 0; Mismatches 0;

QY 7 CF 8
 ||
 Db 1 CF 2

RESULT 8
 SAP_STOVA STANDARD; PRT; 9 AA.
 AC P24547;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Sperm-activating peptide (SAP).
 OS Stomopneustes variolaris (Sea urchin).
 CC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
 CC Echinoidea; Euechinoidea; Diadematoidea; Phymosomatoida; Stomechinidae;
 CC Stomopneustes.
 CC NCBI_TaxID=7663;

RN SEQUENCE, AND DISULFIDE BOND.
 RC TISSUE=Egg jelly; PubMed=1756858;
 RX MEDLINE=92097763; PubMed=1756858;
 RA Yoshino K.-I., Takao T., Shimomishi Y., Suzuki N.;
 RT "Determination of the amino acid sequence of an intramolecular
 RT disulfide linkage-containing sperm-activating peptide by tandem mass
 RT spectrometry";
 RL FEBS Lett. 294:179-182(1991).
 CC -!- FUNCTION: Cause stimulation of sperm respiration and motility
 CC through intracellular alkalization, transient elevations of
 CC cAMP, cGMP and calcium levels in sperm cells, and transient
 CC activation and subsequent inactivation of the membrane form of
 CC guanylate cyclase.
 FT DISULFID 3
 FT SEQUENCE 9 AA; 1010 MW; C469B3387B076EB9 CRC64;
 SQ SEQUENCE 9 AA; 1010 MW; C469B3387B076EB9 CRC64;
 Query Match 23.1%; Score 15; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05; Indels 0; Gaps 0;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 8 FC 9
 DB 2 FC 3
 RESULT 9
 ID DSIP RABIT STANDARD; PRT; 9 AA.
 AC P01158;
 DT 21-JUN-1986 (Rel. 01, Created)
 DT 21-JUN-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Delta sleep-inducing peptide (DSIP).
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OC NCBI_TaxID=9986;
 [1]
 RP SEQUENCE.
 RX MEDLINE=77185324; PubMed=862769;
 RA Monnier M., Dudler L., Gachter R., Maier P.F., Tobler H.J.,
 RA Schoenenberger G.A.;
 RT "The delta sleep inducing peptide (DSIP). Comparative properties of
 RT the original and synthetic nonapeptide.";
 RL Experientia 33:548-552(1977).
 [2]
 RP SEQUENCE, AND SYNTHESIS.
 RX MEDLINE=87175129; PubMed=3550726;
 RA Graf M.V., Kastin A.J.;
 RA Schoenenberger G.A., Maier P.F., Tobler H.J., Wilson K., Monnier M.;
 RT "The delta EEG (sleep)-inducing peptide (DSIP). XI. Amino-acid
 RT analysis, sequence, synthesis and activity of the nonapeptide.";
 RL Pflugers Arch. 376:119-129(1978).
 [3]
 RP REVIEW.
 RX MEDLINE=87175129; PubMed=3550726;
 RA Graf M.V., Kastin A.J.;
 RA Schoenenberger G.A., Maier P.F., Tobler H.J., Wilson K., Monnier M.;
 RT "The delta EEG (sleep)-inducing peptide (DSIP): an update.";
 RL Peptides 7:1165-1187(1986).
 CC -!- FUNCTION: When infused into the mesodiencephalic ventricle of
 CC recipient rabbits induces spindle and delta EEG activity and
 CC reduced motor activities.
 CC -!- MISCELLANEOUS: This peptide was obtained from dialysates of
 CC occipital venous sinus blood from rabbits kept asleep by electric
 CC stimulation of the thalamus.
 CC -!- DATABASE: NAME-Protein Spotlight;
 CC NOTE-Issue 8 of March 2001;
 CC WWW="http://www.expasy.org/spotlight/articles/spot008.html".
 DR PIR; A01422; QDRB.
 SQ SEQUENCE 9 AA; 849 MW; DDD365BDDAA8787D CRC64;
 Query Match 20.0%; Score 13; DB 1; Length 9;
 Best Local Similarity 40.0%; Pred. No. 1.4e+05; Indels 0; Gaps 0;

Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 2 DCRGD 6
 DB 5 DASGE 9
 RESULT 10
 ID TAL1 PICJA STANDARD; PRT; 9 AA.
 AC P17410;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Transaldolase I (EC 2.2.1.2) (Fragment).
 OS Pichia jadinii (Yeast) (Candida utilis).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Pichia.
 OC NCBI_TaxID=4903;
 [1]
 RP SEQUENCE.
 RX MEDLINE=77110646; PubMed=556924;
 RA Sun S.C., Joris L., Tsolas O.;
 RT "Purification of crystallization of transaldolase isozyme I and
 RT evidence for different genetic origin of isozymes I and III in
 RT Candida utilis.";
 RL Arch. Biochem. Biophys. 178:69-78(1977).
 CC -!- FUNCTION: Transaldolase is important for the balance of
 CC metabolites in the pentose-phosphate pathway.
 CC -!- CATALYTIC ACTIVITY: Sedoheptulose 7-phosphate + D-glyceraldehyde
 CC 3-phosphate = D-erythrose 4-phosphate + D-fructose 6-phosphate.
 CC -!- PATHWAY: Pentose phosphate pathway; nonoxidative part.
 CC -!- SIMILARITY: Belongs to the transaldolase family. Subfamily 1.
 DR PIR; A12872; A12872.
 DR InterPro; IPR001585; Transaldolase.
 DR PROSITE; PS00958; TRANSALDOLASE_2; PARTIAL.
 DR PROSITE; PS01054; TRANSALDOLASE_1; PARTIAL.
 DR Transferase; Pentose shunt.
 FT NON_TER 1
 FT NON_TER 9
 FT NON_TER 1
 SQ SEQUENCE 9 AA; 1008 MW; 274F31AFOEB1E058 CRC64;
 Query Match 20.0%; Score 13; DB 1; Length 9;
 Best Local Similarity 50.0%; Pred. No. 1.4e+05; Indels 0; Gaps 0;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CD 2
 DB 5 CB 6
 RESULT 11
 ID OCPI OCTMI STANDARD; PRT; 4 AA.
 AC P58648;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Cardioactive peptides Ocp-1/Ocp-2.
 OS Octopus minor (Octopus).
 OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Necroleoidea;
 OC Octopodiformes; Octopoda; Incirrata; Octopodidae; Octopus.
 OC NCBI_TaxID=89766;
 [1]
 RP SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION.
 RP TISSUE=Brain;
 RX MEDLINE=20336815; PubMed=10876044;
 RA Iwakoshi E., Hisada M., Minakata H.;
 RT "Cardioactive peptides isolated from the brain of a Japanese octopus,
 RT Octopus minor.";
 RL Peptides 21:623-630(2000).
 CC -!- FUNCTION: Cardioactive; has both positive chronotropic and
 CC inotropic effects on the heart. Ocp-2 is a 1000 time less

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CC active than Ocp-1.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- PTM: Ocp-2 has L-Phe instead of D-Phe.
CC -!- MASS SPECTROMETRY: MW=395.2; METHOD=WALDI.
KW Hormone; D-amino acid.
FT MOD RES 2 2 D-PHENYLALANINE (IN OCP-1).
SQ SEQUENCE 4 AA; 394 MW; 6AA879C810000000 CRC64;

Query Match 18.5%; Score 12; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GD 6
DB 3 GD 4

RESULT 12
UXA4_CHLTR STANDARD; PRT; 5 AA.
AC P38005;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Unknown protein from 2D-page from elementary body (Fragment).
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;
RN [1]
RC STRAIN=12/434/Bu;
RA Bini L., Santucci A., Magi B., Marzocchi B., Sanchez-Campillo M.,
RA Comanducci M., Christianen G., Birkelund S., Vretou E., Ratti G.,
RA Pallini V.;
RL Submitted (SEP-1994) to Swiss-Prot.
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 4.5, ITS MW IS: 28 kDa.
DR Sienna-2DPAGE; P38005; -.
FT NON TER 5
SQ SEQUENCE 5 AA; 474 MW; 75BAA865AA800000 CRC64;

Query Match 18.5%; Score 12; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GD 6
DB 3 GD 4

RESULT 13
PPH2_LYCES STANDARD; PRT; 7 AA.
AC P83379;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Purple acid phosphatase isozyme LpSAP2 (EC 3.1.3.2) (Fragment).
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RC SEQUENCE CATALYTIC ACTIVITY, SUBUNIT, SUBCELLULAR LOCATION, AND
RP GLYCOSYLATION.
RC STRAIN=cv. Moneymaker; TISSUE=Seed;
RX MEDLINE=22361242; PubMed=12473124;
RA Bozzo G.G., Raghothama K.G., Plaxton W.C.;
RT "Purification and characterization of two secreted purple acid
RT phosphatase isozymes from phosphate-starved tomato (Lycopersicon
RT esculentum) cell cultures."
RL Eur. J. Biochem. 269:6278-6286 (2002).

CC -!- CATALYTIC ACTIVITY: An orthophosphoric monoester + H(2)O = an
CC alcohol + phosphate.
CC -!- SUBUNIT: Monomer.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- PTM: Glycosylated.
CC -!- MISCELLANEOUS: In L. esculentum there are at least two isozymes of
KW purple acid phosphatase.
KW Hydrolase; Glycoprotein.
FT NON TER 1
FT NON TER 7
SQ SEQUENCE 7 AA; 810 MW; 672AA862C9C729A0 CRC64;

Query Match 18.5%; Score 12; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GD 6
DB 5 GD 6

RESULT 14
ACI_THUAL STANDARD; PRT; 8 AA.
ID ACI_THUAL
AC P18591;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-NOV-1990 (Rel. 16, Last annotation update)
DE Angiotensin-converting enzyme inhibitor.
OS Thunus albacares (Yellowfin tuna) (Neothunnus macropterus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
OC Scombridae; Thunnus.
OX NCBI_TaxID=8236;
RN [1]
RC SEQUENCE.
RC TISSUE=Muscle;
RX MEDLINE=88326322; PubMed=3415688;
RA Kohama Y., Matsumoto S., Oka H., Teramoto T., Okabe M., Mimura T.;
RT "Isolation of angiotensin-converting enzyme inhibitor from tuna
RT muscle."
RL Biochem. Biophys. Res. Commun. 155:332-337 (1988).
DR EIR; A31570; A31570.
SQ SEQUENCE 8 AA; 953 MW; 6AA863733051F1B7 CRC64;

Query Match 18.5%; Score 12; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GD 6
DB 7 GD 8

RESULT 15
FARL_PENMO STANDARD; PRT; 8 AA.
ID FARL_PENMO
AC P83316;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE FMRFamide-like neuropeptide FLP1 (GDRNFLRF-amide).
OS Penaeus monodon (Penaeid shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC Penaeidae; Penaeus.
OX NCBI_TaxID=6687;
RN [1]
RC SEQUENCE, AND MASS SPECTROMETRY.
RP TISSUE=Eyestalk;
RX MEDLINE=21956277; PubMed=11959015;
RA Sithigorngul P., Pupum J., Krungkarn C., Longyant S.,

```

RA Chaivisuthangkura P., Sithigorngul W., Petsom A.;
RT "Seven novel FMRFamide-like neuropeptide sequences from the eyestalk
of the giant tiger prawn Penaeus monodon.";
RL Comp. Biochem. Physiol. 131B:325-337(2002).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- MASS SPECTROMETRY: MW=1024.8; METHOD=MALDI.
CC -1- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
family.
DR GO: GO:0007218; P:neuropeptide signaling pathway; TAS.
KW Neuropeptide; Amidation.
FT MOD_RES 8
SQ SEQUENCE 8 AA; 1024 MW; 72D40729C4540AA8 CRC64;
Query Match 18.5%; Score 12; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GD 6
Db 1 GD 2

Search completed: July 11, 2004, 09:23:55
Job time : 12 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 11, 2004, 09:20:57 ; Search time 38 Seconds
(without alignments)
74.728 Million cell updates/sec

Title: US-09-734-628-1

Perfect score: 65

Sequence: 1 CDCRGDCFC 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 840

Minimum DB seq length: 0

Maximum DB seq length: 9

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:
1: sp_archaea:
2: sp_bacteria:
3: sp_fungi:
4: sp_human:
5: sp_invertebrate:
6: sp_mammal:
7: sp_mbc:
8: sp_organelle:
9: sp_phase:
10: sp_plant:
11: sp_rodent:
12: sp_virus:
13: sp_vertebrate:
14: sp_unclassified:
15: sp_rvirus:
16: sp_bacteriap:
17: sp_archaeap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	36.9	8	Q9TRY3	Q9try3 sus sp. ins
2	22	33.8	9	O12096	O12096 caprine art
3	22	33.8	9	O12100	O12100 caprine art
4	22	33.8	9	O12102	O12102 caprine art
5	22	33.8	9	O12098	O12098 caprine art
6	22	33.8	9	O12104	O12104 caprine art
7	19.5	30.0	9	Q9SF22	Q9sf22 cicer ariet
8	19.5	30.0	9	Q9SF04	Q9sf04 mus musculus
9	19	29.2	7	O55184	O55184 rattus norv
10	17	26.2	8	Q9BY15	Q9by15 homo sapien
11	17	26.2	8	Q9BF82	Q9bf82 ursus arcto
12	17	26.2	8	Q9BFC2	Q9bfc2 macropus eu
13	17	26.2	8	Q9BF90	Q9bf90 tragelaphus
14	17	26.2	8	Q9BFB1	Q9bfb1 echinops te
15	17	26.2	8	Q9BF93	Q9bf93 megaptera n
16	17	26.2	8	Q9BFA1	Q9bfa1 ateles fusc

17	17	26.2	8	Q9BF87	Q9bf87 tapirus ind
18	17	26.2	8	Q9BF89	Q9bf89 euphractus
19	17	26.2	8	Q9BF88	Q9bf88 chaetophrac
20	17	26.2	8	Q9BFA0	Q9bfa0 macaca mula
21	17	26.2	8	Q9BFA8	Q9bfa8 loxodonta a
22	17	26.2	8	Q9BFA9	Q9bfa9 procavia ca
23	17	26.2	8	Q9BFB2	Q9bfb2 sorex arane
24	17	26.2	8	Q9BFB5	Q9bfb5 erinaceus c
25	17	26.2	8	Q9BFB6	Q9bfb6 myrmecophag
26	17	26.2	8	Q9BFB3	Q9bfb3 condylura c
27	17	26.2	8	Q9BF88	Q9bf88 equus cabal
28	17	26.2	8	Q9BF95	Q9bf95 roussettus l
29	17	26.2	8	Q9BF99	Q9bf99 hylobates c
30	17	26.2	8	Q9BF84	Q9bf84 panthera on
31	17	26.2	8	Q9BFC3	Q9bfc3 didelphis m
32	17	26.2	8	Q9BFA4	Q9bfa4 tupia mino
33	17	26.2	8	Q9BFA2	Q9bfa2 tarsius ban
34	17	26.2	8	Q9BF85	Q9bf85 leopardus p
35	17	26.2	8	Q9BFC1	Q9bfc1 choleopus h
36	17	26.2	8	Q9BF89	Q9bf89 okapia john
37	17	26.2	8	Q9BF96	Q9bf96 peropus gi
38	17	26.2	8	Q9BF80	Q9bf80 trichechus
39	17	26.2	8	Q9BF86	Q9bf86 falls silve
40	17	26.2	8	Q9BF92	Q9bf92 tursiops tr
41	17	26.2	8	Q9BF87	Q9bf87 tamandua te
42	17	26.2	8	Q9BF91	Q9bf91 hippopotamu
43	17	26.2	8	Q9BFB4	Q9bfb4 talpa altai
44	17	26.2	8	Q9BFC0	Q9bfc0 choleopus d
45	17	26.2	8	Q9BF98	Q9bf98 callimico g

ALIGNMENTS

RESULT 1
Q9TRY3 PRELIMINARY; PRT; 8 AA.
AC Q9TRY3;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Insulin-like growth factor-binding protein-6, IGFBP-6 (Fragment).
OS Sus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OC NCBI_TaxID=9826;
RN [1]
RP SEQUENCE.

QX MEDLINE=92049376; PubMed=1719383;
RA Shimasaki S., Gao L., Shimomura M., Ling N.;
RT "Isolation and molecular cloning of insulin-like growth factor-binding
RT protein-6."
RL Mol. Endocrinol. 5:938-948(1991).
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 850 MW; 9FB2CEA37EA7687D CRC64;

Query Match 36.9%; Score 24; DB 6; Length 8;
Best Local Similarity 60.0%; Pred. No. 1e+06;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 GDCFC 9
Db 2 GPCWC 6

RESULT 2
O12096 PRELIMINARY; PRT; 9 AA.
ID O12096
AC O12096;
DT 01-JUL-1997 (TRENBLrel. 04, Created)
DT 01-JUL-1997 (TRENBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)

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DE Tat protein (Fragment).
GN TAT.
OS Caprine arthritis encephalitis virus (CAEV).
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11660;
[1]
RN SEQUENCE FROM N.A.
RP Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
RT "dUTPase minus CAEV is attenuated for pathogenesis and accumulates G
to A substitutions.";
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U81439; AAB60832.1; -.
FT NON_TER 1
SQ SEQUENCE 9 AA; 922 MW; 21B8644EB7340EB8 CRC64;

Query Match 33.8%; Score 22; DB 15; Length 9;
Best Local Similarity 75.0%; Pred. No. 1e+06;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CDCR 4
DB 1 CGCR 4

RESULT 3
ID O12100 PRELIMINARY; PRT; 9 AA.
AC O12100;
DT 01-JUL-1997 (TREMELrel. 04, Created)
DT 01-JUL-1997 (TREMELrel. 04, Last sequence update)
DT 01-DEC-2001 (TREMELrel. 19, Last annotation update)
DE Tat protein (Fragment).
GN TAT.
OS Caprine arthritis encephalitis virus (CAEV).
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11660;
[1]
RN SEQUENCE FROM N.A.
RP Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
RT "dUTPase minus CAEV is attenuated for pathogenesis and accumulates G
to A substitutions.";
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U81441; AAB60836.1; -.
FT NON_TER 1
SQ SEQUENCE 9 AA; 922 MW; 21B8644EB7340EB8 CRC64;

Query Match 33.8%; Score 22; DB 15; Length 9;
Best Local Similarity 75.0%; Pred. No. 1e+06;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CDCR 4
DB 1 CGCR 4

RESULT 4
ID O12102 PRELIMINARY; PRT; 9 AA.
AC O12102;
DT 01-JUL-1997 (TREMELrel. 04, Created)
DT 01-JUL-1997 (TREMELrel. 04, Last sequence update)
DT 01-DEC-2001 (TREMELrel. 19, Last annotation update)
DE Tat protein (Fragment).
GN TAT.
OS Caprine arthritis encephalitis virus (CAEV).
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11660;
[1]
RN SEQUENCE FROM N.A.
RP Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
RT "dUTPase minus CAEV is attenuated for pathogenesis and accumulates G
to A substitutions.";
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U81442; AAB60838.1; -.
FT NON_TER 1
SQ SEQUENCE 9 AA; 922 MW; 21B8644EB7340EB8 CRC64;

Query Match 33.8%; Score 22; DB 15; Length 9;
Best Local Similarity 75.0%; Pred. No. 1e+06;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CDCR 4
DB 1 CGCR 4

RESULT 5
ID O12098 PRELIMINARY; PRT; 9 AA.
AC O12098;
DT 01-JUL-1997 (TREMELrel. 04, Created)
DT 01-JUL-1997 (TREMELrel. 04, Last sequence update)
DT 01-DEC-2001 (TREMELrel. 19, Last annotation update)
DE Tat protein (Fragment).
GN TAT.
OS Caprine arthritis encephalitis virus (CAEV).
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11660;
[1]
RN SEQUENCE FROM N.A.
RP Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
RT "dUTPase minus CAEV is attenuated for pathogenesis and accumulates G
to A substitutions.";
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U81440; AAB60835.1; -.
FT NON_TER 1
SQ SEQUENCE 9 AA; 922 MW; 21B8644EB7340EB8 CRC64;

Query Match 33.8%; Score 22; DB 15; Length 9;
Best Local Similarity 75.0%; Pred. No. 1e+06;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CDCR 4
DB 1 CGCR 4

RESULT 6
ID O12104 PRELIMINARY; PRT; 9 AA.
AC O12104;
DT 01-JUL-1997 (TREMELrel. 04, Created)
DT 01-JUL-1997 (TREMELrel. 04, Last sequence update)
DT 01-DEC-2001 (TREMELrel. 19, Last annotation update)
DE Tat protein (Fragment).
GN TAT.
OS Caprine arthritis encephalitis virus (CAEV).
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11660;
[1]
RN SEQUENCE FROM N.A.
RP Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
RT "dUTPase minus CAEV is attenuated for pathogenesis and accumulates G
to A substitutions.";
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U81443; AAB60840.1; -.
FT NON_TER 1
SQ SEQUENCE 9 AA; 922 MW; 21B8644EB7340EB8 CRC64;

Query Match 33.8%; Score 22; DB 15; Length 9;
Best Local Similarity 75.0%; Pred. No. 1e+06;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CDCR 4
DB 1 CGCR 4

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RESULT 7
 ID Q9FSZ2 PRELIMINARY; PRT; 9 AA.
 AC Q9FSZ2;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein (Fragment).
 OS Cicer arietinum (Chickpea) (Garbanzo).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Cicereae; Cicer.
 OX NCBI_TaxID=3827;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Castellana; TISSUE=Etisolated epicotyl;
 RA Dopicio B., Jimenez T., Labrador E.;
 RT "cDNA clones expressed in etiolated Cicer arietinum epicotyls.";
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ299069; CAC10216.1; -.
 KW Hypothetical protein. 1
 FT NON_TER 1
 SQ SEQUENCE 9 AA; 990 MW; 9441BDAA7272EBE CRC64;
 Query Match 30.0%; Score 19.5; DB 10; Length 9;
 Best Local Similarity 55.6%; Pred. No. 1e+06;
 Matches 5; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
 Qy 1 CDCRGD-CF 8
 Db 1 CCCLLDACF 9

RESULT 8
 ID Q99JF4 PRELIMINARY; PRT; 9 AA.
 AC Q99JF4;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE Oct-1L (Fragment).
 GN OCT-1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pankratova E.V., Deyev I.B., Zhenilo S.V., Polanovsky O.L.;
 RT "Tissue-specific Oct-1 isoforms from murine lymphocytes.";
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ310124; CAC34946.1; -.
 FT NON_TER 9
 SQ SEQUENCE 9 AA; 998 MW; 540BCEB5B5BAA7 CRC64;
 Query Match 30.0%; Score 19.5; DB 11; Length 9;
 Best Local Similarity 66.7%; Pred. No. 1e+06;
 Matches 4; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
 Qy 2 DCRGDC 7
 Db 3 DC-SDC 7

RESULT 9
 ID O55184 PRELIMINARY; PRT; 7 AA.
 AC O55184;
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Orphan receptor TR4-NS (Fragment).
 GN TR4.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RX MEDLINE=96198747; PubMed=8612486;
 RA Yoshikawa T., Makino S., Gao X.M., Xing G.Q., Chuang D.M.,
 RA Detera-Wadleigh S.D.;
 RT "Splice variants of rat TR4 orphan receptor: differential expression
 of novel sequences in the 5'-untranslated region and C-terminal
 domain.";
 RL Endocrinology 137:1562-1571 (1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RX MEDLINE=96299786; PubMed=86611150;
 RA Yoshikawa T., Dupont B.R., Leach R.J., Detera-Wadleigh S.D.;
 RT "New variants of the human and rat nuclear hormone receptor, TR4:
 expression and chromosomal localization of the human gene.";
 RL Genomics 35:361-366 (1996).
 DR EMBL; U59454; AAB91433.1; -.
 DR GO: GO:0004872; F:receptor activity; IEA.
 KW Receptor.
 FT NON_TER 1
 SQ SEQUENCE 7 AA; 663 MW; 6DDAA8787B50350 CRC64;

Query Match 29.2%; Score 19; DB 11; Length 7;
 Best Local Similarity 75.0%; Pred. No. 1e+06;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 3 CRGD 6
 Db 3 CGGD 6

RESULT 10
 ID Q9BYV5 PRELIMINARY; PRT; 8 AA.
 AC Q9BYV5;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE cAMP responsive element moderator (Fragment).
 GN CREM.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21082082; PubMed=11214319;
 RA Murphy W.J., Sizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
 RA O'Brien S.J.;
 RT "Molecular phylogenetics and the origins of placental mammals.";
 RL Nature 409:614-618 (2001).
 DR EMBL; AY011664; AAG47575.1; -.
 DR GO: GO:0005634; C:nucleus; NAS.
 DR GO: GO:0003677; F:DNA binding; NAS.
 DR GO: GO:0006355; F:regulation of transcription, DNA-dependent; NAS.
 FT NON_TER 1
 SQ SEQUENCE 8 AA; 1006 MW; DF02C331EBAB572A CRC64;

Query Match 26.2%; Score 17; DB 4; Length 8;
 Best Local Similarity 50.0%; Pred. No. 1e+06;
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 6 DCFC 9
 Db 1 DLIC 4

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RESULT 11
Q9BF82 ID Q9BF82 PRELIMINARY; PRT; 8 AA.
AC Q9BF82;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE CAMP responsive element moderator (Fragment).
GN CREM.
OS Ursus arctos (Brown bear) (Grizzly bear).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.
OX NCBI_TaxID=9644;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21082082; PubMed=11214319;
RA Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RA O'Brien S.J.;
RT "Molecular phylogenetics and the origins of placental mammals.";
RL Nature 409:614-618 (2001).
DR EMBL; AY011621; AAG47536.1; -.
FT NON_TER 1
SQ SEQUENCE 8 AA; 978 MW; DF1DD331EEAB572A CRC64;

Query Match 26.2%; Score 17; DB 6; Length 8;
Best Local Similarity 50.0%; Pred. No. 1e+06;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 DCFC 9
Db 1 DLYC 4

RESULT 12
Q9BFC2 ID Q9BFC2 PRELIMINARY; PRT; 8 AA.
AC Q9BFC2;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE CAMP responsive element moderator (Fragment).
GN CREM.
OS Macropus eugenii (Tamar wallaby).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
OX NCBI_TaxID=9315;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21082082; PubMed=11214319;
RA Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RA O'Brien S.J.;
RT "Molecular phylogenetics and the origins of placental mammals.";
RL Nature 409:614-618 (2001).
DR EMBL; AY011621; AAG47536.1; -.
FT NON_TER 1
SQ SEQUENCE 8 AA; 978 MW; DF1DD331EEAB572A CRC64;

Query Match 26.2%; Score 17; DB 6; Length 8;
Best Local Similarity 50.0%; Pred. No. 1e+06;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 DCFC 9
Db 1 DLYC 4

RESULT 13
Q9BF90 ID Q9BF90 PRELIMINARY; PRT; 8 AA.
AC Q9BF90;
DT 01-JUN-2001 (TReMBLrel. 17, Created)

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DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE CAMP responsive element moderator (Fragment).
GN CREM.
OS Tragelaphus eurycerus (Bongo).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Tragelaphus.
OX NCBI_TaxID=69297;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21082082; PubMed=11214319;
RA Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RA O'Brien S.J.;
RT "Molecular phylogenetics and the origins of placental mammals.";
RL Nature 409:614-618 (2001).
DR EMBL; AY011673; AAG47583.1; -.
FT NON_TER 1
SQ SEQUENCE 8 AA; 978 MW; DF1DD331EEAB572A CRC64;

Query Match 26.2%; Score 17; DB 6; Length 8;
Best Local Similarity 50.0%; Pred. No. 1e+06;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 DCFC 9
Db 1 DLYC 4

RESULT 14
Q9BFB1 ID Q9BFB1 PRELIMINARY; PRT; 8 AA.
AC Q9BFB1;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE CAMP responsive element moderator (Fragment).
GN CREM.
OS Echinops telfairi (Lesser hedgehog tenrec).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Insectivora; Tenrecidae; Tenrecinae; Echinops.
OX NCBI_TaxID=9371;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21082082; PubMed=11214319;
RA Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RA O'Brien S.J.;
RT "Molecular phylogenetics and the origins of placental mammals.";
RL Nature 409:614-618 (2001).
DR EMBL; AY011632; AAG47547.1; -.
FT NON_TER 1
SQ SEQUENCE 8 AA; 978 MW; DF1DD331EEAB572A CRC64;

Query Match 26.2%; Score 17; DB 6; Length 8;
Best Local Similarity 50.0%; Pred. No. 1e+06;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 DCFC 9
Db 1 DLYC 4

RESULT 15
Q9BF93 ID Q9BF93 PRELIMINARY; PRT; 8 AA.
AC Q9BF93;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE CAMP responsive element moderator (Fragment).
GN CREM.
OS Megaptera novaeangliae (Humpback whale).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```


OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Mysticeti;
OC Balaeonopteridae; Megaptera.
OX NCBI_TaxID=9773;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21082082; PubMed=11214319;
RA Murphy W.J., Elzirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RA O'Brien S.J.;
RT "Molecular phylogenetics and the origins of placental mammals."
RL Nature 409:614-618(2001).
DR EMBL; AY011669; AAG47580.1; -.
FT NON TER 1
SQ SEQUENCE 8 AA; 1025 MW; DF02C3240EAB572A CRC64;

Query Match 26.2%; Score 17; DB 6; Length 8;
Best Local Similarity 50.0%; Pred.No. 1e+06;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 6 DCF 9
| : |
Db 1 DLIC 4

Search completed: July 11, 2004, 09:24:46
Job time : 39 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 11, 2004, 10:04:38 ; Search time 52 Seconds
(without alignments)
48.902 Million cell updates/sec

Title: US-09-734-628-1

Perfect score: 65

Sequence: 1 CDCRGBCFC 9

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 49

Minimum DB seq length: 0

Maximum DB seq length: 9

Post-processing: Minimum Match 100%

Maximum Match 100%

Listing first 500 summaries

Database :

A_Geneseq_29Jan04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	65	100.0	9	2 AAR76200	AlphaV/beta3
2	65	100.0	9	2 AAR76200	AlphaV/beta3
3	65	100.0	9	2 AAR76200	AlphaV/beta3
4	65	100.0	9	2 AAR76200	AlphaV/beta3
5	65	100.0	9	2 AAR76200	AlphaV/beta3
6	65	100.0	9	2 AAR76200	AlphaV/beta3
7	65	100.0	9	2 AAR76200	AlphaV/beta3
8	65	100.0	9	2 AAR76200	AlphaV/beta3
9	65	100.0	9	2 AAR76200	AlphaV/beta3
10	65	100.0	9	2 AAR76200	AlphaV/beta3
11	65	100.0	9	2 AAR76200	AlphaV/beta3
12	65	100.0	9	2 AAR76200	AlphaV/beta3
13	65	100.0	9	2 AAR76200	AlphaV/beta3
14	65	100.0	9	2 AAR76200	AlphaV/beta3
15	65	100.0	9	2 AAR76200	AlphaV/beta3
16	65	100.0	9	2 AAR76200	AlphaV/beta3
17	65	100.0	9	2 AAR76200	AlphaV/beta3
18	65	100.0	9	2 AAR76200	AlphaV/beta3
19	65	100.0	9	2 AAR76200	AlphaV/beta3
20	65	100.0	9	2 AAR76200	AlphaV/beta3
21	65	100.0	9	2 AAR76200	AlphaV/beta3
22	65	100.0	9	2 AAR76200	AlphaV/beta3
23	65	100.0	9	2 AAR76200	AlphaV/beta3
24	65	100.0	9	2 AAR76200	AlphaV/beta3
25	65	100.0	9	2 AAR76200	AlphaV/beta3

26	65	100.0	9	5 ABB72945	Integrin
27	65	100.0	9	5 ABB72961	Integrin
28	65	100.0	9	5 ABJ04359	BRASIL me
29	65	100.0	9	5 AB08066	Cyclic RG
30	65	100.0	9	5 ABG70729	avB3 bind
31	65	100.0	9	5 ABG70729	avB3 bind
32	65	100.0	9	5 ABE17983	Human lig
33	65	100.0	9	5 ABE17983	Human lig
34	65	100.0	9	5 ABG70754	Targeting
35	65	100.0	9	5 AAU75609	Synthetic
36	65	100.0	9	5 AAU79138	Synthetic
37	65	100.0	9	5 AAU98972	Adeno-ass
38	65	100.0	9	5 AAU98972	Adeno-ass
39	65	100.0	9	5 ABG79525	Tumour-ta
40	65	100.0	9	5 ABG79525	Tumour-ta
41	65	100.0	9	5 ABG31063	Alpha v b
42	65	100.0	9	5 AAG78427	Cyclic pe
43	65	100.0	9	5 AAM51995	Drug targ
44	65	100.0	9	6 ABG73024	Integrin
45	65	100.0	9	6 ABG73024	Integrin
46	65	100.0	9	6 ABG73024	Integrin
47	65	100.0	9	6 ABG73024	Integrin
48	65	100.0	9	6 ABG73024	Integrin
49	65	100.0	9	7 ADC44955	Endotheli

ALIGNMENTS

RESULT 1

AAR76200

ID AAR76200 standard; peptide; 9 AA.

XX AAR76200;

XX 24-JAN-1996 (first entry)

XX AlphaV/beta3 and alphaV/beta5 integrin binding peptide #4.

XX High affinity; integrin binding peptide; alphas/betal; alphav/betas;

XX alphav/betas; RGD; stable configuration; wound healing;

XX osteoclast attachment; bone; angiogenesis; metastasis; tumour;

XX smooth muscle cell migration.

XX Synthetic.

XX WC9514714-AA.

XX 01-JUN-1995.

XX 22-NOV-1994; 94WO-US013542.

XX 24-NOV-1993; 93US-00158001.

XX 04-AUG-1994; 94US-00286861.

XX (JOL-) LA JOLLA CANCER RES FOUND.

XX Ruoslatti E, Koivunen E;

XX WPI; 1995-206899/27.

XX High affinity integrin binding peptides - can be used to attach cells to

XX a substrate, inhibit the attachment of osteoclasts to bone, promote wound

XX healing, inhibit angiogenesis, metastasis of tumours and migration of

XX smooth muscle cells.

XX Claim 21; Page 62; 86pp; English.

XX The sequences given in AAR76185-200 and AAR9073-94 are high affinity

XX integrin binding peptides which bind to various integrins. Peptides which

XX bind to alphas/betal integrins contain the motifs given in AAR76185-86

XX and peptides which bind to alphav/beta3 integrins

XX contain the motif given in AAR76187. Alphav/beta5 integrins are also

CC bound by RGD containing peptides. These peptides assume a
 CC conformationally stabilised configuration which is due to the formation
 CC of a disulphide bond, a peptide bond or a lactam bond. These peptides may
 CC be used for isolating the complementary integrin from a sample mixture by
 CC contacting them under ionic conditions to allow binding of the integrin
 CC to the peptide and then separating the integrin from the peptide. They
 CC can be used for attaching cells to a substrate, by binding them to the
 CC substrate with the cell. The peptides promote wound healing when applied
 CC locally and inhibit the attachment of osteoclasts to bone. They inhibit
 CC angiogenesis, metastasis of tumours and migration of smooth muscle cells
 XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 65; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDCRGDCFC 9
 |||||
 DB 1 CDCRGDCFC 9

RESULT 2
 AAW60289
 ID AAW60289 standard; peptide; 9 AA.

XX AC AAW60289;
 XX DT 24-AUG-1998 (first entry)
 XX DE Tumour homing peptide of the invention.
 XX KW Tumour homing peptide; in vivo panning;
 KW alpha-V-containing integrin binding motif; tumour.
 XX OS Unidentified.
 XX PN WO9810795-A2.
 XX PD 19-MAR-1998.
 XX PF 10-SEP-1997; 97WO-US016086.
 XX PR 10-SEP-1996; 96US-00710067.
 XX PA (BURN-) BURNHAM INST.
 XX PI Ruoslahti E, Pasqualini R;
 XX DR WPI; 1998-207151/18.
 XX PT Tumour homing molecules and their conjugates - useful for, e.g. directing
 PT linked moiety to tumour containing angiogenic vasculature.
 XX PS Claim 6; Page 91; 105pp; English.

XX The present peptide represents a tumour homing peptide, and is produced
 CC by in vivo panning. The peptide has an alpha-V-containing integrin
 CC binding motif, Arg-Gly-Asp (RGD). The in vivo panning comprises
 CC administering a library of diverse peptides to a subject having a tumour,
 CC collecting a sample of the tumour, identifying a peptide that homes to
 CC the tumour, collecting a sample of normal tissue corresponding to the
 CC tumour, and determining that the peptide that homes to the tumour is not
 CC present in the normal tissue. The tumour homing peptide can be linked to
 CC a moiety (e.g. doxorubicin), and used to direct the moiety to a tumour
 XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 65; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDCRGDCFC 9
 |||||
 DB 1 CDCRGDCFC 9

Db 1 CDCRGDCFC 9
 |||||
 RESULT 3
 AAW56034
 ID AAW56034 standard; peptide; 9 AA.
 XX AC AAW56034;
 XX DT 29-JUL-1998 (first entry)
 XX DE Chimeric adenovirus fiber protein non-native amino acid sequence 3.

XX KW Chimeric; adenovirus; fiber protein; binding; targeting; coat protein;
 KW constrained peptide motif; gene therapy; cancer; heart disease;
 KW autoimmune disorder.
 XX OS Synthetic.
 OS Mastadenovirus.
 XX PN WO9807865-A1.
 XX PD 26-FEB-1998.
 XX PF 21-AUG-1997; 97WO-US014719.
 XX PR 21-AUG-1996; 96US-00701124.
 XX PA (GENV-) GENVEC INC.

XX PI Wickham TJ, Roelvink PW, Kovesdi I;
 XX DR WPI; 1998-169169/15.
 XX PT Chimeric adenovirus fibre proteins - containing non-native amino acid
 PT sequence to provide for binding and entry into cells, especially for gene
 therapy.
 XX PS Claim 7; Page 68; 124pp; English.

XX The present sequence represents a specifically claimed non-native amino
 CC acid sequence from a chimeric adenovirus fibre protein (AFP) of the
 CC present invention. The non-native amino acid sequence allows the chimeric
 CC fibre (or a vector comprising the chimeric fibre) to more efficiently
 CC bind to and enter cells. The products can be used for gene therapy, for
 CC treating cancer, e.g. melanoma, glioma and lung cancers as well as
 CC genetic disorders, e.g. cystic fibrosis, haemophilia and muscular
 CC dystrophy as well as pathogenic infections, e.g. HIV, tuberculosis and
 CC hepatitis and also for heart disease, to e.g. prevent restenosis
 CC following angioplasty or to promote angiogenesis to reperfuse necrotic
 CC tissue, and in autoimmune disorders, e.g. Crohn's disease, colitis,
 CC rheumatoid arthritis, and Alzheimer's disease
 XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 65; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDCRGDCFC 9
 |||||
 DB 1 CDCRGDCFC 9

RESULT 4
 AAY42255
 ID AAY42255 standard; peptide; 9 AA.
 XX AC AAY42255;
 XX DT 01-DEC-1999 (first entry)
 XX

DE XX Synthetic RGD-4C peptide.
 KW Adenovirus; gene therapy; coxsackievirus adenovirus receptor; CAR;
 KW cancer; cystic fibrosis; muscular dystrophy.
 XX
 OS Synthetic.
 PN WO9939734-A1.
 PD 12-AUG-1999.
 XX
 PF 05-FEB-1999; 99WO-US002549.
 XX
 PR 06-FEB-1998; 98US-0073947P.
 PR 10-SEP-1998; 98US-0099801P.
 XX
 PA (UABR-) UAB RES FOUND.
 XX
 PI Curriel DT, Krasnykh VN, Dmitriev I;
 XX
 DR WPI; 1999-539951/45.
 XX
 PT Recombinant adenovirus vectors with modified fiber knob loops, useful in
 PT gene therapy.
 XX
 PS Example 21; Page 49; 126pp; English.

XX This sequence represents a synthetic RGD-4C peptide. DNA encoding this
 CC sequence was cloned into the sequence encoding the HI loop of the
 CC adenovirus fibre protein knob domain. This was then used in the
 CC construction of plasmids encoding a modified fibre protein. Recombinant
 CC adenovirus genomes were generated by homologous DNA recombination in E.
 CC coli, before excision of the newly generated genome for virus rescue. The
 CC knob domain of the adenovirus fibre protein mediates the initial binding
 CC and recognition of the coxsackievirus and adenovirus receptor (CAR) on
 CC the cell surface. The HI loop protrudes from the knob domain and connects
 CC beta-strands involved in the formation of the cell binding site.
 CC Recombinant adenovirus vectors are used in a number of gene therapy
 CC applications; however, the reliance on the CAR means that in certain
 CC situations, recombinant viruses are sequestered by high CAR-expressing
 CC non-target cells while the true target cells, if low in CAR, receive
 CC little of the therapeutic gene. Modification of the HI loop by
 CC replacement of the hypervariable region of the loop with a peptide such
 CC as the RGD peptide results in the ability of the virus to utilise an
 CC alternative receptor during the cell entry process. Modifying the
 CC adenovirus fibre knob protein in this way increases the ability of an
 CC adenovirus to transduce a tumour cell in vitro, in vivo and ex vivo. The
 CC vector Ad5HIFLAG incorporating an RGD peptide demonstrated two to three
 CC orders of magnitude of increased gene transfer to ovarian cancer cells.
 CC The modified adenovirus has an altered tropism, which allows the
 CC adenovirus to be targeted to selected cell types. The recombinant
 CC adenovirus can be used to provide gene therapy for individuals suffering
 CC from cancer, cystic fibrosis and Duchenne's muscular dystrophy

XX SQ Sequence 9 AA;

Query Match 100.0%; Score 65; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDCRGDCFC 9
 |||||
 Db 1 CDCRGDCFC 9

RESULT 5
 AAY43233
 ID AAY43233 standard; peptide; 9 AA.
 XX
 AC AAY43233;
 XX

DT 13-JAN-2000 (first entry)
 XX

DE XX RGD-containing peptide #12.

XX Nucleic acid delivery vehicle; bifunctional complex; transgene; CFTR;
 KW cell surface targeting; cell surface molecule binding region; integrin;
 KW cystic fibrosis transmembrane regulator; alphas-antitrypsin;
 KW suicide gene; beta-glucocerebrosidase; cell transfection; cell infection;
 KW RGD peptide.
 XX

OS Synthetic.

PN WO9940214-A2.

PD 12-AUG-1999.

PF 08-FEB-1999; 99WO-US002680.

XX 09-FEB-1998; 98US-00020483.

PR 09-FEB-1998; 98US-0135092P.

PR 06-NOV-1998; 98US-0107471P.

XX (GENZ) GENZYME CORP.

XX O'riordan C, Romanczuk H, Wadsworth SC;

XX WPI; 1999-610583/52.

XX Nucleic acid delivery vehicles useful for transfecting and infecting a

PT target cell.

PS Claim 22; Page 39; 118pp; English.

XX This sequence represents a RGD-containing peptide that can be used in a
 CC bifunctional complex used in the nucleic acid delivery vehicle (I) of the
 CC invention. (I) is for transfecting and/or infecting a target cell, and
 CC comprises a transgene and a bifunctional complex (B) that targets the
 CC nucleic acid delivery vehicle to the cell surface. (B) comprises a
 CC delivery vehicle binding portion, a cell surface molecule binding portion
 CC (such as this sequence) and a linker connecting them. The delivery
 CC vehicle can be specifically targeted to the cell via the binding to cell
 CC surface molecules. (I) can be used to target cells, which express
 CC integrins such as, HT-29 colon carcinoma cells, lymphocytes and
 CC monocytes, blood platelets, SMC-90 human lung fibroblast, MG(63)
 CC osteosarcoma cell line, vascular endothelial cells and melanoma cells.
 CC (I) is useful for delivery of nucleic acids encoding CFTR (cystic
 CC fibrosis transmembrane regulator), alphas-antitrypsin, beta-
 CC glucocerebrosidase and suicide genes. The construct increases the
 CC efficiency of cellular uptake of (I). The constructs also enable the
 CC transfection/infection of cells that are normally refractory to
 CC transfection/infection by targeting cell receptors that are present on
 CC such cells

XX SQ Sequence 9 AA;

Query Match 100.0%; Score 65; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDCRGDCFC 9
 |||||
 Db 1 CDCRGDCFC 9

RESULT 6
 AAW93626
 ID AAW93626 standard; protein; 9 AA.

XX

AC AAW93626;

XX 28-JUN-1999 (first entry)

DE NGR receptor binding tumour homing peptide 5.

XX Tumour homing peptide; tumour; diagnosis; endothelial cell;

XX Albritton LM, Zavorotinskaya T;
 XX WPI; 2000-116313/10.
 XX Novel isolated nucleic acid, useful for gene therapy.
 XX Example 10; Page 84; 190pp; English.
 XX The specification describes mutant retrovirus envelope proteins. The
 CC envelope protein coding sequence can be mutated to encode a mutant
 CC envelope protein with a substitution of one or more amino acids in at
 CC least one motif of the retrovirus protein. The mutant protein fragment
 CC allows for decreased shedding of the surface protein by suppressing
 CC precursor cleavage and increase envelope stability and fusion of
 CC retroviruses with cell membranes, while maintaining mutant envelope
 CC protein incorporation into a virion, and viral titers of about two orders
 CC of magnitude within that observed for wild-type retrovirus when the
 CC protein or fragment is expressed on the surface of a retroviral particle.
 CC The proteins have an increased ability to penetrate targets, typically
 CC cells and a correspondingly increased ability to deliver nucleic acids or
 CC drugs. The mutated nucleic acid is useful for gene and drug therapy,
 CC especially as drug delivery vehicles. The retrovirus particles can be
 CC utilized to transduce eukaryotic cells. The transduced cells are useful
 CC in the treatment of cancer in a human. Other diseases contemplated for
 CC treatment include adenosine deaminase deficiency (ADA), thalassemia,
 CC hemophilia, diabetes, alpha-anti trypsin deficiency, brain and neural
 CC disorders, phenylketonuria, growth disorders, heart diseases and immune
 CC diseases. The present sequence was used in the course of the invention,
 CC to quantitate targeted retroviral vector gene delivery in vivo

XX SQ Sequence 9 AA;
 Query Match 100.0%; Score 65; DB 3; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDCRGDCFC 9
 |||||
 DB 1 CDCRGDCFC 9

RESULT 9
 AAY44970
 ID AAY44970 standard; protein; 9 AA.
 AC AAY44970;
 XX 23-MAY-2000 (first entry)
 DT RGD-4C targeting sequence for KDEL receptor inhibitor protein.
 DE KDEL receptor inhibitor; heat shock protein; immune response;
 KW oligomerisation domain; neoplasia; sarcoma; lymphoma; leukaemia;
 KW melanoma; carcinoma; glioblastoma; astrocytoma; oncogene;
 KW infectious disease; allergy; autoimmune disease.
 XX Unidentified.
 OS WO200006729-A1.
 FN 10-FEB-2000.
 XX 28-JUL-1999; 99WO-US017147.
 PF 29-JUL-1998; 98US-00124671.
 PR (SLOK) SLOAN KETTERING INST CANCER RES.
 XX Rothman JE, Mayhew M, Hoe MH;
 PI WPI; 2000-195296/17.
 XX

PT Inhibitors of the KDEL receptor which comprises an oligomerization domain
 PT useful for promoting secretion of proteins which are normally retained
 PT within the cell.
 XX Disclosure; Page 17; 87pp; English.
 XX The patent discloses the use of KDEL receptor inhibitor to promote
 CC secretion of proteins that are normally retained within the cell such as
 CC heat shock proteins by inhibiting KDEL receptor-mediated return of
 CC protein complexes to endoplasmic reticulum. This makes the secreted heat
 CC shock proteins more accessible to the immune system and improves immune
 CC response to a target antigen. The inhibitor protein comprises several
 CC subunits where each subunit comprises an oligomerization domain and has
 CC at its carboxy terminus a region which binds to a KDEL receptor. The
 CC target antigen may be associated with diseases including neoplasia such
 CC as sarcoma, lymphoma, leukemia, melanoma, carcinoma, glioblastoma and
 CC astrocytoma, with defective tumour suppressor genes, oncogenes,
 CC infectious diseases, allergy or autoimmune diseases. The present sequence
 CC is a targeting peptide termed RGD-4C. This may be incorporated into the
 CC amino terminal region of a KDEL receptor inhibitor protein downstream
 CC from a cleavably removed sequence to improve its activity or alter its
 CC immunogenicity

XX SQ Sequence 9 AA;
 Query Match 100.0%; Score 65; DB 3; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDCRGDCFC 9
 |||||
 DB 1 CDCRGDCFC 9

RESULT 10
 AAB17928
 ID AAB17928 standard; peptide; 9 AA.
 XX AAB17928;
 AC 31-OCT-2000 (first entry)
 DT TPO-mimetic peptide sequence SEQ ID NO:1032.
 DE Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
 KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
 KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP;
 KW inhibitor; erythropoietin; thrombopoietin; interleukin 1;
 KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
 KW vascular endothelial growth factor; matrix metalloproteinase; asthma;
 KW thrombosis; pharmaceutical.
 XX Synthetic.
 OS WO2000024782-A2.
 FN 04-MAY-2000.
 XX 25-OCT-1999; 99WO-US025044.
 PF 23-OCT-1998; 98US-0105371P.
 PR 22-OCT-1999; 99US-00428082.
 XX (AMGE-) AMGEN INC.
 XX Feige U, Liu C, Cheetham J, Boone TC;
 PI WPI; 2000-350702/30.
 XX Novel composition of matter comprising an Fc domain and pharmacologically
 PT active peptides, useful for treating cancer and autoimmune diseases.
 XX Disclosure; Page 559; 608pp; English.
 PS

XX The present invention describes composition of matter (I) comprising an
 CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
 CC (X1)a-P1-(X2)b, where: P1 = an Fc domain; X1 and X2 = are each
 CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-
 CC (L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2,
 CC P3, and P4 = are each independently sequences of pharmacologically active
 CC peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b,
 CC c, d, e, and f = are each independently 0 or 1, provided that at least 1
 CC of a and b is 1. The composition can have cytostatic, antiasthmatic,
 CC thrombolytic and immunosuppressive activities. DNAs, vectors and host
 CC cells from the present invention can be used for producing pharmaceutical
 CC compositions. The compositions are useful for treating cancer, asthma,
 CC thrombosis, or autoimmune diseases. The use of an Fc domain (rather than
 CC a Fab domain) can provide a longer half-life or incorporate functions
 CC such as Fc receptor binding, protein A binding, complement fixation, and
 CC possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to
 CC AAB18003 represent nucleotide and amino acid sequences used in the
 CC exemplification of the present invention
 XX Sequence 9 AA;

Query Match 100.0%; Score 65; DB 3; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDCRGDCFC 9
 Db 1 CDCRGDCFC 9

RESULT 11
 AAB17964
 ID AAB17964 standard; peptide; 9 AA.

AC AAB17964;

XX 31-OCT-2000 (first entry)

DE Integrin-binding peptide sequence SEQ ID NO:1076.

XX Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
 KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
 KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP;
 KW inhibitor; erythropoietin; thrombopoietin; interleukin 1;
 KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
 KW vascular endothelial growth factor; matrix metalloproteinase; asthma;
 KW thrombosis; pharmaceutical.

OS Synthetic.

XX WO200024782-A2.

XX 04-MAY-2000.

XX 25-OCT-1999; 99WO-US025044.

XX 23-OCT-1998; 98US-0105371P.

XX 22-OCT-1999; 99US-00428082.

XX (AMGE-) AMGEN INC.

XX Feige U, Liu C, Cheetham J, Boone TC;

XX WPI; 2000-350702/30.

XX Novel composition of matter comprising an Fc domain and pharmacologically
 PT active peptides, useful for treating cancer and autoimmune diseases.

XX Claim 39; Page 591; 608pp; English.

XX The present invention describes composition of matter (I) comprising an
 CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:

CC (X1)a-P1-(X2)b, where: P1 = an Fc domain; X1 and X2 = are each
 CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-
 CC (L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2,
 CC P3, and P4 = are each independently sequences of pharmacologically active
 CC peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b,
 CC c, d, e, and f = are each independently 0 or 1, provided that at least 1
 CC of a and b is 1. The composition can have cytostatic, antiasthmatic,
 CC thrombolytic and immunosuppressive activities. DNAs, vectors and host
 CC cells from the present invention can be used for producing pharmaceutical
 CC compositions. The compositions are useful for treating cancer, asthma,
 CC thrombosis, or autoimmune diseases. The use of an Fc domain (rather than
 CC a Fab domain) can provide a longer half-life or incorporate functions
 CC such as Fc receptor binding, protein A binding, complement fixation, and
 CC possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to
 CC AAB18003 represent nucleotide and amino acid sequences used in the
 CC exemplification of the present invention
 XX Sequence 9 AA;

Query Match 100.0%; Score 65; DB 3; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDCRGDCFC 9
 Db 1 CDCRGDCFC 9

RESULT 12
 AAB17346

ID AAB17346 standard; peptide; 9 AA.

AC AAB17346;

XX 31-OCT-2000 (first entry)

XX Integrin-binding peptide sequence SEQ ID NO:450.

XX Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
 KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
 KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP;
 KW inhibitor; erythropoietin; thrombopoietin; interleukin 1;
 KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
 KW vascular endothelial growth factor; matrix metalloproteinase; asthma;
 KW thrombosis; pharmaceutical.

OS Synthetic.

XX WO200024782-A2.

XX 04-MAY-2000.

XX 25-OCT-1999; 99WO-US025044.

XX 23-OCT-1998; 98US-0105371P.

XX 22-OCT-1999; 99US-00428082.

XX (AMGE-) AMGEN INC.

XX Feige U, Liu C, Cheetham J, Boone TC;

XX WPI; 2000-350702/30.

XX Novel composition of matter comprising an Fc domain and pharmacologically
 PT active peptides, useful for treating cancer and autoimmune diseases.

XX Claim 39; Page 354; 608pp; English.

XX The present invention describes composition of matter (I) comprising an
 CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
 CC (X1)a-P1-(X2)b, where: P1 = an Fc domain; X1 and X2 = are each
 CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-
 CC (L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2,

CC P3, and P4 = are each independently sequences of pharmacologically active
 CC peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b,
 CC c, d, e, and f = are each independently 0 or 1, provided that at least 1
 CC of a and b is 1. The composition can have cytostatic, antiasthmatic,
 CC thrombolytic and immunosuppressive activities. DNAs, vectors and host
 CC cells from the present invention can be used for producing pharmaceutical
 CC compositions. The compositions are useful for treating cancer, asthma,
 CC thrombosis, or autoimmune diseases. The use of an Fc domain (rather than
 CC a Fab domain) can provide a longer half-life or incorporate functions
 CC such as Fc receptor binding, protein A binding, complement fixation, and
 CC possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to
 CC AAB18003 represent nucleotide and amino acid sequences used in the
 CC exemplification of the present invention
 XX
 XX Sequence 9 AA;

Query Match 100.0%; Score 65; DB 3; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDCRGDCFC 9
 |||||
 Db 1 CDCRGDCFC 9

RESULT 13

AA90211
 ID AA90211 standard; peptide; 9 AA.

XX
 AC AA90211;

XX
 DT 06-AUG-2003 (revised)
 DT 21-SEP-2000 (first entry)

DE Alphav integrin targeting peptide #1.

XX
 KW Ligand epitope; UPAR; urokinase-type plasminogen activator receptor;
 KW adenovirus; hexon HRV5 loop; hexon HI loop; peripheral artery disease;
 KW recombinant adenovirus vector; tumour; restenosis; gene therapy; asthma;
 KW smooth muscle cell proliferation inhibitor; coronary artery disease;
 KW obesity; neurodegenerative disease; infection; autoimmune disease; HIV;
 KW thrombosis; diabetes; tropism-modified virus.

XX
 OS Synthetic.

XX
 PN WO200012738-A1.

XX
 PD 09-MAR-2000.

XX
 PF 27-AUG-1999; 99WO-IB001524.

XX
 PR 27-AUG-1998; 98US-0098028P.

XX
 PA (AVET) AVENTIS PHARMA SA.

XX
 PI Vigne B, Dedieu J, Latta M, Yeh P, Perricaudet M;

XX
 DR WPI; 2000-256653/22.

XX
 PT Urokinase-type plasminogen activator receptor (UPAR)-targeted adenovirus
 PT vectors having modified hexon HRV5 and HI loops and modified fiber
 PT proteins useful for targeted gene therapy to treat cancer or restenosis.
 XX
 PS Example 5; Page 53; 128pp; English.

XX
 CC This sequence represents an alphav integrin targeting peptide. The
 CC invention relates to an adenovirus from which at least a part of the
 CC hexon HRV5 or HI loop is replaced with a binding peptide, or targeting
 CC sequence, flanked by connecting amino acid spacers, to functionally
 CC display its binding specificity at the capsid surface. The invention also
 CC relates to a recombinant adenovirus vector wherein a binding peptide, or
 CC targeting sequence, is connected to the C-terminus of the fiber by a
 CC connecting spacer, or linker, so as to functionally display its binding

CC specificity at the capsid surface. The adenovirus or recombinant
 CC adenovirus vector can be used to preferentially express a gene in a
 CC target cell, especially a cell that expresses a UPAR. The targeted
 CC adenovirus vector preferably comprises a heterologous gene encoding a
 CC gene for treatment of a tumour or restenosis. The targeted adenovirus
 CC vector is useful for gene therapy treatment of a disease, and for
 CC manufacturing a medicine used in gene therapy treatment of a disease. The
 CC viruses can also be used to inhibit smooth muscle cell proliferation, to
 CC treat peripheral artery diseases, infections, autoimmune diseases, asthma, HIV,
 CC neurodegenerative diseases, diabetes. The viruses are particularly targeted against a
 CC urokinase-type plasminogen activator receptor (UPAR). The adenoviruses
 CC are tropism-modified without adversely impacting productivity of the
 CC vectors. (Updated on 06-AUG-2003 to correct OS field.)
 XX
 XX Sequence 9 AA;

Query Match 100.0%; Score 65; DB 3; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDCRGDCFC 9
 |||||
 Db 1 CDCRGDCFC 9

RESULT 14

AAO22875
 ID AAO22875 standard; peptide; 9 AA.

XX
 AC AAO22875;

XX
 DT 30-JAN-2003 (first entry)

XX
 DE Angiogenic treatment compound related synthetic peptide #75.

XX
 KW Cyclic; cytostatic; antitumour; targeting moiety; chelator; peptide;
 KW peptidomimetic; angiogenesis; metallopharmaceutical; new blood vessel;
 KW rheumatoid arthritis; cancer; cancer planar; SPPECT gamma scintigraphy;
 KW positron emission; X-ray computed tomography; magnetic resonance imaging;
 KW synthetic cyclic peptide.

XX
 OS Synthetic.

XX
 PN WO9558162-A2.

XX
 PD 18-NOV-1999.

XX
 PF 29-MAR-1999; 99WO-US006826.

XX
 PR 31-MAR-1998; 98US-0080150P.

XX
 PR 18-DEC-1998; 98US-0112715P.

XX
 PA (DUPO) DU PONT PHARM CO.

XX
 PI Rajopadhye M, Edwards DS, Harris TD, Heminway SJ, Liu S;
 PI Singh PR;

XX
 DR WPI; 2000-105546/09.

XX
 PT Novel compound for diagnosis and treatment of cancer.

XX
 PS Disclosure; Page 62; 213pp; English.

XX
 CC The invention relates to compounds comprising targeting moiety which is
 CC bound to a chelator. The targeting moiety is a peptide or peptidomimetic
 CC which binds to a receptor and is upregulated during angiogenesis. The
 CC compound has 0-1 linking groups between targeting moiety and the
 CC chelator. The metallopharmaceutical composition is used in treating
 CC rheumatoid arthritis or cancer by imaging the formation of new blood
 CC vessels, imaging cancer planar or SPPECT gamma scintigraphy, positron
 CC emission or X-ray computed tomography or with magnetic resonance imaging.
 CC This sequence represents a synthetic cyclic peptide relating to the novel

```

CC compounds of the invention
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 65; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDCRGDCFC 9
Db 1 CDCRGDCFC 9

RESULT 15
AAB21701
ID AAB21701 standard; peptide; 9 AA.
XX
AC AAB21701;
XX
XX 22-MAR-2001 (first entry)
XX
DE Human breast tumour homing peptide #1.
XX
Cytostatic; homing pro-apoptotic conjugate; tumour; antimicrobial;
KW breast; prostate; melanoma; cancer; Kaposi's sarcoma; human.
XX
OS Homo sapiens.
XX
XX WO200042973-A2.
XX
XX 27-JUL-2000.
XX
XX 21-JAN-2000; 2000WO-US001602.
XX
XX 22-JAN-1999; 99US-00235902.
XX
XX (BURN-) BURNHAM INST.
XX
XX Ellerby HM, Bredesen DE, Pasqualini R, Ruoslahti BI;
PI WPI; 2000-499174/44.
XX
XX Homing pro-apoptotic conjugate comprising a tumor homing molecule that
PT selectively homes to a mammalian cell type or tissue linked to an
PT antimicrobial peptide, useful for the treatment of prostate cancer.
XX
XX Claim 12; Page 105; 118pp; English.
XX
XX The present invention relates to homing pro-apoptotic conjugates,
CC comprising of a tumour homing molecule that selectively homes to a
CC mammalian cell type or tissue, linked to an antimicrobial peptide. The
CC homing pro-apoptotic conjugates are selectively internalised by the
CC mammalian cell type or tissue and exhibits high toxicity, especially to
CC angiogenic vasculature. The antimicrobial peptide has low mammalian cell
CC toxicity when not linked to the tumor homing molecule. The conjugates are
CC useful for the treatment of cancer e.g. Kaposi's sarcoma, breast and
CC prostate cancer or melanoma. The present sequence is a homing peptide
CC isolated in the present invention, which can be conjugated to an
CC antimicrobial peptide to make the homing pro-apoptotic conjugates of the
CC present invention
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 65; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDCRGDCFC 9
Db 1 CDCRGDCFC 9

RESULT 16
AAB21701
ID AAB21701 standard; peptide; 9 AA.
XX
AC AAB21701;
XX
XX 22-MAR-2001 (first entry)
XX
DE Human breast tumour homing peptide #1.
XX
Cytostatic; homing pro-apoptotic conjugate; tumour; antimicrobial;
KW breast; prostate; melanoma; cancer; Kaposi's sarcoma; human.
XX
OS Homo sapiens.
XX
XX WO200042973-A2.
XX
XX 27-JUL-2000.
XX
XX 21-JAN-2000; 2000WO-US001602.
XX
XX 22-JAN-1999; 99US-00235902.
XX
XX (BURN-) BURNHAM INST.
XX
XX Ellerby HM, Bredesen DE, Pasqualini R, Ruoslahti BI;
PI WPI; 2000-499174/44.
XX
XX Homing pro-apoptotic conjugate comprising a tumor homing molecule that
PT selectively homes to a mammalian cell type or tissue linked to an
PT antimicrobial peptide, useful for the treatment of prostate cancer.
XX
XX Claim 12; Page 105; 118pp; English.
XX
XX The present invention relates to homing pro-apoptotic conjugates,
CC comprising of a tumour homing molecule that selectively homes to a
CC mammalian cell type or tissue, linked to an antimicrobial peptide. The
CC homing pro-apoptotic conjugates are selectively internalised by the
CC mammalian cell type or tissue and exhibits high toxicity, especially to
CC angiogenic vasculature. The antimicrobial peptide has low mammalian cell
CC toxicity when not linked to the tumor homing molecule. The conjugates are
CC useful for the treatment of cancer e.g. Kaposi's sarcoma, breast and
CC prostate cancer or melanoma. The present sequence is a homing peptide
CC isolated in the present invention, which can be conjugated to an
CC antimicrobial peptide to make the homing pro-apoptotic conjugates of the
CC present invention
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 65; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDCRGDCFC 9
Db 1 CDCRGDCFC 9

RESULT 17
AAB50242
ID AAB50242 standard; peptide; 9 AA.
XX
AC AAB50242;
XX
XX 13-MAR-2001 (first entry)

```

```

AAB20271
ID AAB20271 standard; peptide; 9 AA.
XX
AC AAB20271;
XX
XX 14-MAY-2001 (first entry)
XX
DE Peptide that specifically targets tumour blood vessels.
XX
XX Tumour; breast carcinoma; Kaposi's sarcoma; melanoma;
KW fiberless radiative effector; therapy; imaging.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FT Misc-difference 4..6 /note= "RGD motif"
FT
XX
XX WO200108660-A2.
XX
XX 08-FEB-2001.
XX
XX 26-JUL-2000; 2000WO-US020292.
XX
XX 02-AUG-1999; 99US-00366314.
XX
XX (UNMI ) UNIV MICHIGAN.
XX
XX Philbert MA, Tjalkens R, Aylott JW, Clark HA, Monson EE;
PI Kopelman R;
XX
XX WPI; 2001-182851/18.
XX
XX Composition for destroying or inhibiting growth of tumor cells and for
PT imaging tumors or other biological targets, has molecular recognition
PT element attached to fiberless radiative effector having a toxic agent.
XX
XX Disclosure; Page 35; 95pp; English.
XX
XX The present sequence is that of a peptide that specifically binds to
CC tumour blood vessels. It includes an RGD motif. The peptide, and
CC conjugates containing it, selectively binds to various tumours, including
CC breast carcinomas, Kaposi's sarcoma and melanoma. The peptide can be
CC used as the molecular recognition element of novel fiberless radiative
CC effectors (FRES) of the invention. The invention is related to cell or
CC pathogen destruction via FRES that encapsulate a radical generator. The
CC FRES include a polymer matrix, a photodynamic or radiodynamic dye which
CC produces free radicals upon stimulation, cloaking material, and at least
CC 1 molecular recognition element for targeting to a biological target,
CC e.g. the present peptide. They are useful in various in vitro and in vivo
CC procedures, destroying or inhibiting the growth of biological targets
CC (pathogens, macromolecules, tumour cells in culture or in the body), in
CC therapies including chemotherapy, radiation therapy, antibiotic and
CC vaccine therapy
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 65; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDCRGDCFC 9
Db 1 CDCRGDCFC 9

RESULT 17
AAB50242
ID AAB50242 standard; peptide; 9 AA.
XX
AC AAB50242;
XX
XX 13-MAR-2001 (first entry)

```

XX Enhanced infectivity adenoviral vector fibre replacement ligand.
 XX Adenoviral vector; gene therapy; infectability;
 KW tumour-specific replication.
 XX Unidentified.
 XX WO200067576-A1.
 XX 16-NOV-2000.
 XX 12-MAY-2000; 2000WO-US013114.
 XX 12-MAY-1999; 99US-0133634P.
 XX (UABR-) UAB RES FOUND.
 XX Curiel DT, Krasnykh VN, Alemany R, Dmitriev I;
 XX WPI; 2001-122702/13.
 XX New infectivity-enhanced, conditionally-replicative adenovirus containing
 PT a modified wild type adenoviral fiber, useful for cancer therapy.
 XX Claim 8; Page 70; 104pp; English.
 XX The present invention provides an adenoviral vector with an enhanced
 CC ability to infect tumour cells and which is conditionally replicative,
 CC enabling replication in only one cell type. This can be used in the gene
 CC therapy treatment of cancers
 XX Sequence 9 AA;
 SQ

Query Match 100.0%; Score 65; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CDCRGDCFC 9
 Db 1 CDCRGDCFC 9

RESULT 18
 AAB97086
 ID AAB97086 standard; peptide; 9 AA.
 XX
 AC AAB97086;
 XX

DT 02-AUG-2001 (first entry)
 XX Integrin-binding peptide #4.
 DE
 KW Integrin; avB3; avB5; analgesic; cytostatic; macrocyclic chelant;
 KW metal chelate formation; metallocoradiopharmaceutical;
 KW magnetic resonance imaging; MRI; disease diagnosis;
 KW systemic radiotherapy; bone pain; bone cancer; antagonist.
 XX
 OS Unidentified.
 XX

XX Key Location/Qualifiers
 FH Modified-site 1
 FT /note= "The amino group of the residue at position 1
 FT forms a peptide bond with the carboxy group of the
 FT residue at position 9 to form a cyclic molecule"
 FT Modified-site 9
 FT /note= "The amino group of the residue at position 1
 FT forms a peptide bond with the carboxy group of the
 FT residue at position 9 to form a cyclic molecule"

XX WO200119838-A1.
 XX 22-MAR-2001.
 PD

XX 07-SEP-2000; 2000WO-US024482.
 XX 13-SEP-1999; 99US-0153512P.
 XX (DUPO) DU PONT PHARM CO.
 XX Liu S;
 XX WPI; 2001-389600/41.
 XX New nitrogen containing macrocyclic chelant compounds used in metal
 PT chelates for e.g. X-ray imaging and for attaching diagnostic and
 PT therapeutic isotopes to biologically active targeting molecules.
 XX Disclosure; Page 72; 121pp; English.
 XX The present sequence is provided in a specification relating to novel
 CC nitrogen containing macrocyclic chelant compounds. The compounds are used
 CC for forming metal chelates used as diagnostic or therapeutic
 CC metallocoradiopharmaceuticals, or magnetic resonance imaging (MRI) contrast
 CC agents. They are also used for attaching metal ions to bio-directing
 CC groups including proteins, peptides, peptidomimetics and non peptides
 CC that bind in vivo to a receptor or enzyme that is expressed or up-
 CC regulated at a site or in a disease state. The metallocoradiopharmaceuticals are
 CC used in disease diagnosis by MRI or in treating disease by systemic
 CC radiotherapy. Radiolanthide chelates with phosphonemethyl and optionally
 CC carboxymethyl groups on the four N atoms can be used for treating bone
 CC pain and bone metastases. The macrocyclic chelants rapidly form stable
 CC metal chelates. The present sequence binds with high affinity to the
 CC integrins avB3 and avB5
 XX Sequence 9 AA;
 SQ

Query Match 100.0%; Score 65; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CDCRGDCFC 9
 Db 1 CDCRGDCFC 9

RESULT 19
 AAE06279
 ID AAE06279 standard; peptide; 9 AA.
 XX
 AC AAE06279;
 XX

DT 25-SEP-2001 (first entry)
 XX Tumour homing peptide used for homing pro-apoptotic conjugates.
 DE
 KW Chimeric prostate-homing pro-apoptotic peptide; prostate-homing peptide;
 KW antimicrobial peptide; prostate cancer; tumour homing molecule;
 KW cytostatic; RGD motif.
 XX
 OS Synthetic.
 XX

PN WO200153342-A1.
 XX 26-JUL-2001.
 PD
 PF 16-JAN-2001; 2001WO-US001362.
 XX
 PR 21-JAN-2000; 2000US-00489582.
 XX (BURN-) BURNHAM INST.
 XX Ruoslahti EI, Pasqualini R, Arap W, Bredesen DE, Ellerby HM;
 XX WPI; 2001-451901/48.
 XX

PT Novel chimeric prostate-homing pro-apoptotic peptide, used to treat
PT prostate cancer, comprises a prostate-homing peptide linked to an
PT antimicrobial peptide.
XX
PS Example 3B; Page 84; 176pp; English.
XX
CC The patent discloses novel chimeric prostate-homing pro-apoptotic peptide
CC which comprises a prostate-homing peptide linked to an antimicrobial
CC peptide, where the chimeric peptide is selectively internalised by and
CC exhibits high toxicity to prostate tissue and where the antimicrobial
CC peptide has low mammalian cell toxicity when not linked to prostate-
CC homing peptide. The chimeric peptide is used to direct an antimicrobial
CC peptide in vivo to a prostate cancer, to induce selective toxicity in
CC vivo in a prostate cancer, and to treat a patient with prostate cancer.
CC The present peptide sequence is a tumour homing molecule containing a RGD
CC motif. This sequence is useful in the homing of pro-apoptotic conjugates
CC of the invention
XX
SQ Sequence 9 AA;
Query Match 100.0%; Score 65; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CDCRGDCFC 9
DB 1 CDCRGDCFC 9
RESULT 20
AAE11044
ID AAE11044 standard; peptide; 9 AA.
AC AAE11044;
XX
XX 18-DEC-2001 (first entry)
XX RGD-containing peptide.
XX Tumour necrosis factor; TNF; cytokine; cytostatic; virucide;
XX TNF related apoptosis inducing ligand; TRAIL; cancer; viral infection;
XX human immunodeficiency virus; HIV; leukaemia; gene therapy; lymphoma;
XX melanoma.
XX Unidentified.
XX US6284236-B1.
XX 04-SEP-2001.
XX 26-MAY-1999; 99US-00320424.
XX 29-JUN-1995; 95US-00496632.
XX 01-NOV-1995; 95US-00548368.
XX 25-JUN-1996; 96US-00670354.
XX 26-MAR-1998; 98US-00048641.
XX 10-NOV-1998; 98US-00190046.
XX (IMV) IMMUNEX CORP.
XX Wiley SR, Goodwin RG;
XX WPI; 2001-595463/67.
XX New tumor necrosis factor related apoptosis inducing ligand polypeptides
XX for treating viral infections (e.g. bovine viral diarrhoea or human
XX immunodeficiency virus), or cancers (e.g. leukemia or lymphoma).
XX Disclosure; Col 11; 41pp; English.
XX The invention relates to a cytokine designated as tumour necrosis factor
XX (TNF) related apoptosis inducing ligand (TRAIL), which induces apoptosis
XX of certain target cells, including cancer cells and virally infected

CC cells. The TRAIL polypeptides are useful in killing cancer cells, in
CC treating viral infections (e.g. bovine viral diarrhoea or human
CC immunodeficiency virus (HIV)) and cancers (e.g. leukaemia, lymphoma and
CC melanoma), as a research reagent useful in studying apoptosis including
CC the regulation of programmed cell death. TRAIL DNA sequences may be
CC employed in developing a gene therapy approach to treating disorders
CC mediated by defective or insufficient amounts of TRAIL, in the production
CC of TRAIL polypeptides and as probes or primers in polymerase chain
CC reactions (PCR). The present sequence is a RGD-containing peptide that
CC binds an integrin associated with tumour. This sequence is used to
CC construct a fusion protein comprising TRAIL protein
XX
SQ Sequence 9 AA;
Query Match 100.0%; Score 65; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CDCRGDCFC 9
DB 1 CDCRGDCFC 9
RESULT 21
AAU98837
ID AAU98837 standard; peptide; 9 AA.
XX AC AAU98837;
XX 22-AUG-2002 (first entry)
XX Tumour homing peptide RGD-4C.
XX Targeting peptide; cancer; tumour targeting; cytostatic; anti-HIV;
XX immunostimulant; immunogen; cancer; human immunodeficiency virus; HIV;
XX vector delivery.
XX Synthetic.
XX WO200220724-A2.
XX 14-MAR-2002.
XX 07-SEP-2001; 2001WO-US028045.
XX 08-SEP-2000; 2000US-0231266P.
XX 17-JAN-2001; 2001US-00765101.
XX (TEXA) UNIV TEXAS SYSTEM.
XX Arap W, Pasqualini R;
XX WPI; 2002-489672/52.
XX Modulation of immune system response comprises administration of
XX targeting peptide attached to immunogen.
XX Disclosure; Page 11; 86pp; English.
XX This invention relates to a method for modulating the immune system
XX response comprising administration of a lymph node targeting peptide
XX attached to an immunogen. The invention also comprises a bispecific
XX compound comprising the sequences Cys-Ala-Tyr or Ser-Cys-Ala-Arg, a
XX bispecific compound comprising a targeting peptide attached to a vector
XX binding moiety and a method for targeting a vector to an organ or tissue
XX comprising administering the vector and a complex comprising a targeting
XX peptide and a binding moiety. The peptides of the invention may have
XX cytostatic, anti-HIV or immunostimulant activities. The method of the
XX invention is useful for increasing the immune response to an immunogen,
XX especially a cancer cell or human immunodeficiency virus (HIV). The
XX method is useful for the selective delivery of gene therapy vectors. The
XX present sequence represents an tumour homing peptide RGD-4C used in the
XX method of the invention

```

XX SQ Sequence 9 AA;
Query Match 100.0%; Score 65; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDCRGDCFC 9
Db 1 CDCRGDCFC 9

RESULT 22
ABG35079
ID ABG35079 standard; peptide; 9 AA.
AC ABG35079;
XX
XX
XX 15-JUL-2002 (first entry)
DT
XX
XX RGD-4C-beta gal phage transduction inhibitor peptide.
DE
XX
XX Targeting peptide; cancer; Hodgkin's disease; cytostatic;
KW immunosuppressive; anti-inflammatory; antiarthritic; antiviral;
KW antiatherosclerotic; antidiabetic; antibacterial; diabetes mellitus;
KW inflammatory disease; arthritis; atherosclerosis; cancer;
KW autoimmune disease; bacterial infection; viral infection.
XX
XX Synthetic.
OS
XX WO200220722-A2.
PN
XX
XX 14-MAR-2002.
PD
XX
XX 07-SEP-2001; 2001WO-US027702.
PF
XX
XX 08-SEP-2000; 2000US-0231266P.
PR
XX 17-JAN-2001; 2001US-00765101.
PR
XX (TEXA ) UNIV TEXAS SYSTEM.
PA
XX
XX Arap W, Pasqualini R;
PI
XX WPI; 2002-383050/41.
XX
XX Identifying targeting peptides useful for treating e.g. diabetes
PT mellitus, inflammatory diseases, cancer, or autoimmune diseases,
PT comprises exposing a sample to a phage display library and recovering
PT phage bound to the sample.
PS Disclosure; Page 262; 298pp; English.
XX
XX This invention relates to a novel method for identifying disease
CC targeting peptides. The method comprises exposing a sample from an organ,
CC tissue or cell type of interest, to a phage display library and
CC recovering phage bound to the sample (the phage expresses targeting
CC peptides). The peptides identified by the method of the invention may
CC have cytostatic, immunosuppressive, anti-inflammatory, antithrombotic,
CC antiatherosclerotic, antidiabetic, antibacterial, antiviral
CC activities. The methods and composition are useful for identifying
CC targeting peptides and one or more receptors for a targeting peptide. The
CC targeting peptides are used for selective delivery of therapeutic agents,
CC including gene therapy vectors and fusion proteins, to specific organs,
CC tissues, or cell types in subject. The targeting peptide may also be used
CC for treating diseases such as diabetes mellitus, inflammatory diseases,
CC arthritis, atherosclerosis, cancer, autoimmune diseases, bacterial and
CC viral infections and Hodgkin's disease. The present sequence represents a
CC targeting peptide of the invention
XX
XX Sequence 9 AA;
Query Match 100.0%; Score 65; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDCRGDCFC 9
Db 1 CDCRGDCFC 9

RESULT 23
AAU81110
ID AAU81110 standard; peptide; 9 AA.
XX
XX AAU81110;
AC
XX
XX 09-APR-2002 (first entry)
DT
XX
XX Integrin-antagonist peptide #17.
DE
XX
XX IGG Fc; anticoagulant; thrombolytic; cytostatic; antiinflammatory;
KW immunosuppressive; osteopathic; antagonist; laminin; saw-scaled viper;
KW echistatin; integrin; selectin; vinculin; platelet aggregation;
KW angiogenesis; tumour; inflammation; autoimmune disease;
KW rheumatoid arthritis; osteoporosis.
XX
XX Synthetic.
OS
XX WO200181377-A2.
PN
XX
XX 01-NOV-2001.
PD
XX
XX 23-APR-2001; 2001WO-US013069.
PF
XX
XX 21-APR-2000; 2000US-0198919P.
PR
XX 03-MAY-2000; 2000US-0201394P.
PR
XX (AMGE-) AMGEN INC.
PA
XX
XX Feige U, Kohno T, Lacey DL, Boone TC;
PI
XX WPI; 2002-062025/08.
XX
XX Composition comprising integrin or adhesion antagonistic peptide and
PT vehicle, useful for treating or preventing platelet aggregation, has a
PT longer half-life than free peptide.
XX
XX Claim 11; Page 19; 68pp; English.
XX
XX The invention relates to a composition comprising an integrin/adhesion
CC antagonistic peptide (I) and a vehicle e.g. IGG Fc. The peptides are
CC based on laminin or saw-scaled viper echistatin and target integrin,
CC selectin or vinculin. Also included are compounds of formula (Ia) and
CC their multimers (X1)a-F1-1-(X2)b where; F1 = Fc domain; X1 and X2 =
CC -(L1)c-P1-1, (L1)c-P1-1-(L2)d-P2, (L1)c-P1-1-(L2)d-P2-(L3)e-
CC P3 or (L1)c-P1-1-(L2)d-P2-(L3)e-P3-1-(L4)f-P4; P1-P4 = same or
CC different (I); L1-L4 = same or different linkers; a-f = 0 or 1,
CC provided at least one of a and b = 1, a nucleic acid that encodes (Ia),
CC an expression vector containing the nucleic acid, host cells containing
CC the vector, producing a pharmaceutically active compound (B) by
CC covalently linking at least one Fc domain to at least one amino acid
CC sequence of a selected randomized (I) and any of six laminin-related
CC peptides (Ib). The compositions are used prophylactically and
CC therapeutically in the same way as (I), e.g. to inhibit platelet
CC aggregation or angiogenesis (tumours), or to treat inflammation and
CC autoimmune diseases (e.g. rheumatoid arthritis) and many different forms
CC of osteoporosis, also for diagnosis. Attaching the vehicle (especially Fc
CC domain) to (I) increases the half-life (free (I) are normally degraded
CC very quickly in vivo). The present sequence is an antagonist peptide of
CC the invention
XX
XX Sequence 9 AA;
Query Match 100.0%; Score 65; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```


RESULT 26
 ABB72945
 ID ABB72945 standard; peptide; 9 AA.
 XX AC ABB72945;
 XX DT 05-APR-2002 (first entry)
 XX DE Integrin binding peptide SEQ ID NO:450.
 XX KW Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG; EPO;
 KW erythropoietin; TPO; tumour necrosis factor alpha inhibitor;
 KW TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TMP;
 KW TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist;
 KW MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;
 KW cytosolic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;
 KW antianemic; anorectic; antiinfertility; haemostatic; dermatological;
 KW neuroprotective; inflammatory disease; autoimmune disease; tumour growth;
 KW cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;
 KW sleep disorder; neurological degenerative disease; anaemia;
 KW thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
 KW Fanconi's syndrome.
 XX OS Homo sapiens.
 OS Synthetic.
 XX WO200183525-A2.
 XX PD 08-NOV-2001.
 XX PF 02-MAY-2001; 2001WO-US014310.
 XX PR 03-MAY-2000; 2000US-00563286.
 XX PA (AMGE-) AMGEN INC.
 XX PI Feige U, Liu C, Cheetham JC, Boone TC, Gudas JM;
 XX WPI; 2002-130313/17.
 XX Novel vehicle-peptide molecule or its multimers useful for treating
 PT inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,
 PT diabetic retinopathy, obesity, sleep disorders and infertility.
 XX Claim 39; Page 47; 176pp; English.
 XX The present invention describes a vehicle-peptide molecule (I) or its
 CC multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,
 CC cytosolic, antirheumatic, antiarthritic, antidiabetic, ophthalmological,
 CC antianemic, anorectic, antiinfertility, haemostatic, dermatological and
 CC neuroprotective activities. (I) can be used as a therapeutic or
 CC prophylactic agent as well as for screening purposes. (I) is useful for
 CC diagnosing diseases characterised by dysfunction of their associated
 CC protein of interest, for identifying normal or abnormal proteins of
 CC interest, as a part of diagnostic kit to detect the presence of their
 CC proteins of interest in a biological sample. Additionally, (I) is useful
 CC for treating inflammatory and autoimmune diseases, tumour growth, cancer,
 CC rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,
 CC infertility, and neurological degenerative diseases. (I), comprising EPO-
 CC mimetic compounds are useful for treating disorders characterised by low
 CC red blood cell levels such as anaemia. The EPO-mimetic comprising
 CC compounds are useful for treating conditions that involve an existing
 CC megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet
 CC deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic
 CC tumour which result in thrombocytopaenia, systemic lupus erythematosus,
 CC and Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777
 CC represent amino acid and nucleic acid sequences used in the
 CC exemplification of the present invention
 XX Sequence 9 AA;
 XX Query Match 100.0%; Score 65; DB 5; Length 9;
 XX Best Local Similarity 100.0%; Pred. No. 1.4e+06;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CDCRGDCFC 9
 Db 1 CDCRGDCFC 9
 RESULT 27
 ABB72961
 ID ABB72961 standard; peptide; 9 AA.
 XX AC ABB72961;
 XX DT 05-APR-2002 (first entry)
 XX DE Integrin binding peptide SEQ ID NO:1076.
 XX KW Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG; EPO;
 KW erythropoietin; TPO; tumour necrosis factor alpha inhibitor;
 KW TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TMP;
 KW TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist;
 KW MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;
 KW cytosolic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;
 KW antianemic; anorectic; antiinfertility; haemostatic; dermatological;
 KW neuroprotective; inflammatory disease; autoimmune disease; tumour growth;
 KW cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;
 KW sleep disorder; neurological degenerative disease; anaemia;
 KW thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
 KW Fanconi's syndrome.
 XX OS Homo sapiens.
 OS Synthetic.
 XX WO200183525-A2.
 XX PD 08-NOV-2001.
 XX PF 02-MAY-2001; 2001WO-US014310.
 XX PR 03-MAY-2000; 2000US-00563286.
 XX PA (AMGE-) AMGEN INC.
 XX PI Feige U, Liu C, Cheetham JC, Boone TC, Gudas JM;
 XX WPI; 2002-130313/17.
 XX Novel vehicle-peptide molecule or its multimers useful for treating
 PT inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,
 PT diabetic retinopathy, obesity, sleep disorders and infertility.
 XX Claim 39; Page 47; 176pp; English.
 XX The present invention describes a vehicle-peptide molecule (I) or its
 CC multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,
 CC cytosolic, antirheumatic, antiarthritic, antidiabetic, ophthalmological,
 CC antianemic, anorectic, antiinfertility, haemostatic, dermatological and
 CC neuroprotective activities. (I) can be used as a therapeutic or
 CC prophylactic agent as well as for screening purposes. (I) is useful for
 CC diagnosing diseases characterised by dysfunction of their associated
 CC protein of interest, for identifying normal or abnormal proteins of
 CC interest, as a part of diagnostic kit to detect the presence of their
 CC proteins of interest in a biological sample. Additionally, (I) is useful
 CC for treating inflammatory and autoimmune diseases, tumour growth, cancer,
 CC rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,
 CC infertility, and neurological degenerative diseases. (I), comprising EPO-
 CC mimetic compounds are useful for treating disorders characterised by low
 CC red blood cell levels such as anaemia. The EPO-mimetic comprising
 CC compounds are useful for treating conditions that involve an existing
 CC megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet
 CC deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic
 CC tumour which result in thrombocytopaenia, systemic lupus erythematosus,
 CC and Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777
 CC represent amino acid and nucleic acid sequences used in the
 CC exemplification of the present invention

CC represent amino acid and nucleic acid sequences used in the
CC exemplification of the present invention

XX Sequence 9 AA;

Query Match 100.0%; Score 65; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDCRGDCFC 9
| | | | |
Db 1 CDCRGDCFC 9

RESULT 28
ABU04359
ID ABU04359 standard; peptide; 9 AA.

XX AC ABU04359;
XX DT 24-OCT-2002 (first entry)
XX DE BRASIL method-related peptide 3.

XX KW BRASIL; targeting peptide; bacterial infection;
XX KW Biopanning and Rapid Analysis of Selective Interactive Ligands; diabetes;
XX KW inflammatory arthritis; atherosclerosis; cancer; autoimmune disease;
XX KW viral infection; cardiovascular disease; degenerative disease.

XX OS Unidentified.

XX PN WO200220822-A2.

XX PD 14-MAR-2002.

XX PF 07-SEP-2001; 2001WO-US028124.

XX PR 08-SEP-2000; 2000US-0231266P.

XX PR 17-JAN-2001; 2001US-00765101.

XX PA (TEXA) UNIV TEXAS SYSTEM.

XX PI Arap W, Pasqualini R;

XX DR WPI; 2002-404697/43.

XX PT Identification of targeting peptides that can be used to treat diseases
e.g. cancer and arthritis, by the BRASIL (Biopanning and Rapid Analysis
of Selective Interactive Ligands) method comprises a single differential
centrifugation step.

XX PS Example 1; Page 57; 167pp; English.

XX CC The invention comprises a method (BRASIL - Biopanning and Rapid Analysis
of Selective Interactive Ligands) to obtain a targeting peptide. The
BRASIL method of the invention involves: exposing a target to a phage
display library in a first phase; exposing the first phase to a second
phase; and separating the phage bound to the target from unbound phage.
The BRASIL method of the invention allows cell phages to be separated
from the remaining unbound phage in a single differential centrifugation
step. When compared to conventional cell panning methods, the BRASIL
method shows a significant increase in recovery of specific phage and a
substantial decrease in background. The BRASIL method is useful for
identifying targeting peptides. The targeting peptides identified by the
method of the invention are useful for treating disease states, such as:
diabetes; inflammatory arthritis; atherosclerosis; cancer; autoimmune
disease; bacterial infection; viral infection; cardiovascular disease and
degenerative disease. The present amino acid sequence represents a
peptide that was used in the method of the invention

XX SQ Sequence 9 AA;

Query Match 100.0%; Score 65; DB 5; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDCRGDCFC 9
| | | | |
Db 1 CDCRGDCFC 9

RESULT 29
ABB08066
ID ABB08066 standard; peptide; 9 AA.

XX AC ABB08066;

XX DT 27-AUG-2002 (first entry)

XX DE Cyclic RGD (cRGD) targeting ligand domain.

XX KW Targeting molecule; adenoviral receptor domain; trimerisation; cancer;
XX KW coxsackie-adenovirus receptor; CAR; transmembrane protein; cytostatic;
XX KW hepatotropic; virucide; gene therapy; RGD; cRGD; cyclic.

XX OS Homo sapiens.

XX PN WO200229072-A2.

XX PD 11-APR-2002.

XX PF 05-OCT-2001; 2001WO-EP011514.

XX PR 06-OCT-2000; 2000US-00684552.

XX PR 08-OCT-2000; 2000US-0327562P.

XX PA (NOVS) NOVARTIS AG.

XX PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.

XX PI Kim JG, Smith T, Stevenson SC, Kaleko M;

XX DR WPI; 2002-471317/50.

XX PT A targeting molecule for use in forming complexes to treat cancer, such
as adenocarcinoma of the prostate, comprises a soluble adenoviral
receptor domain, a trimerization domain and a targeting ligand domain.

XX PS Example 2; Page 32; 75pp; English.

XX CC The invention relates to a targeting molecule that comprises a soluble
adenoviral receptor domain, a trimerisation domain and a targeting ligand
domain. The targeting molecules are used for targeting an adenoviral
particle to a cell expressing a cell surface molecule. The method
involves contacting the adenoviral particle with the targeting molecule
to form a complex, and contacting the cell with the complex, and in
delivering a heterologous gene selectively to a cell. The complex is used
for preparing a medicament for treatment of disease in a human mammal,
such as cancer, preferably, adenocarcinoma of the prostate, by gene
therapy. The present sequence represents a cyclic RGD (cRGD) targeting
ligand domain, used in the targeting molecule of the invention

XX SQ Sequence 9 AA;

Query Match 100.0%; Score 65; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDCRGDCFC 9
| | | | |
Db 1 CDCRGDCFC 9

RESULT 30
ABG70729
ID ABG70729 standard; peptide; 9 AA.

XX

AC ABG70729;
 DT 27-NOV-2002 (first entry)
 XX
 DE avB3 binding cyclic peptide #4.
 XX
 KW Macrocytic chelant; pathological process; angiogenic neovasculature;
 KW contrast agent; X-ray; CT; computerised tomography; magnetic resonance;
 KW radiopharmaceutical; cardiovascular disorder; infectious disease; cancer;
 KW imaging; hypoxia; apoptosis; cardiac ischaemia; thrombosis; infection;
 KW inflammation; restenosis; atherosclerosis; diabetic retinopathy;
 KW macular degeneration; wound healing; reperfusion injury; cytostatic;
 KW heavy metal detoxification; avB3; cyclic; circular.
 XX
 OS Synthetic.
 XX
 XX US2002098149-A1.
 PN
 XX 25-JUL-2002.
 PD
 XX 27-DEC-2001; 2001US-00033765.
 PF
 XX 09-JAN-2001; 2001US-0260500P.
 PR
 XX (LIUS/) LIU S.
 PA
 XX Liu S;
 PI
 XX WPI; 2002-706013/76.
 DR
 XX New macrocytic chelants and metal chelates useful for treating e.g.
 PT pathological processes involving angiogenic neovasculature and as
 PT contrast agents.
 PT
 XX Disclosure; Page 11; 21pp; English.
 PS
 XX The present invention relates to new macrocytic chelants. The invention
 CC can be used for treating pathological processes involving angiogenic
 CC neovasculature and as contrast agents in X-ray, CT (computerised
 CC tomography), magnetic resonance and radiopharmaceuticals for the
 CC diagnosis of cardiovascular disorders, infectious disease and cancer, and
 CC for imaging hypoxia, apoptosis, cardiac ischaemia, thrombosis, infection,
 CC inflammation, restenosis, atherosclerosis, diabetic retinopathy, macular
 CC degeneration, wound healing and reperfusion injury. The invention is also
 CC useful for heavy metal detoxification. The present amino acid sequence
 CC represents a cyclic peptide that was used in the methods of the invention
 CC to bind to avB3
 XX
 SQ Sequence 9 AA;
 Query Match 100.0%; Score 65; DB 5; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CDCRGDCFC 9
 Db 1 CDCRGDCFC 9
 RESULT 31
 ABB76442
 ID ABB76442 standard; peptide; 9 AA.
 XX
 XX ABB76442;
 AC
 XX 02-SEP-2002 (first entry)
 DT
 XX RGD-4C Peptide with integrin binding affinity.
 DE
 XX Integrin; adenovirus; vector; cancer; tumour; gene therapy.
 KW
 XX Synthetic.
 OS
 XX

PN US2002058045-A1.
 XX
 PD 16-MAY-2002.
 XX
 PF 01-MAY-2001; 2001US-00845160.
 XX
 XX 31-MAY-2000; 2000JP-00161577.
 PR
 XX 27-APR-2001; 2001JP-00131688.
 PR
 XX (NAHE-) NAT INST HEALTH SCI.
 PA
 XX Mizuguchi H, Hayakawa T;
 PI WPI; 2002-499507/53.
 DR N-PSDB; ABR83749.
 DR
 XX A method for constructing a fiber-mutant adenovirus vector in which a
 PT foreign peptide is introduced by a simple system into the fiber HI loop-
 PT coding gene of adenovirus providing a more effective means of introducing
 PT foreign peptides.
 PT
 XX Example 1; Page 4; 13pp; English.
 PS
 XX The present sequence is that of an RGD-4C peptide having binding affinity
 CC to cell surface integrins. DNA encoding a foreign peptide, such as the
 CC present sequence, may be introduced into a fibre HI loop-coding gene
 CC sequence using a method of the invention for construction of fibre-mutant
 CC adenovirus vectors. The fibre HI loop comprises amino acids 537-549 of a
 CC fibre molecule. Insertion of a foreign peptide into this region does not
 CC affect the formation of trimers by the fibre molecules. A claimed method
 CC for constructing a fibre-mutant adenovirus vector comprises inserting a
 CC unique restriction enzyme recognition sequence, especially Csp45I and/or
 CC ClaI, into the fibre HI loop-encoding sequence, and introducing a foreign
 CC peptide-encoding DNA into the gene sequence. The peptide preferably
 CC includes the tripeptide Arg-Gly-Asp (RGD) or Asn-Gly-Arg (NGR) and has
 CC tropism for tumour vascular endothelial cells. Selection of RGD-4C as the
 CC foreign peptide can improve the efficiency of gene introduction not only
 CC to adenovirus-sensitive cells but also to e.g. CHO cells, respiratory
 CC epidermal cells, smooth muscle cells, vascular endothelial cells, T-
 CC cells, macrophages, haematopoietic stem cells, dendritic cells and cancer
 CC cells which are CAR-negative but which express integrins on their
 CC surfaces, e.g. human glioma LN444 cells. A synthetic oligonucleotide
 CC encoding the peptide and including Csp45I and ClaI restriction sites can
 CC be ligated directly into the HI loop-coding gene sequence digested with
 CC the corresponding restriction enzymes. The fiber-mutant adenovirus vector
 CC has high gene transfer efficiency
 XX
 SQ Sequence 9 AA;
 Query Match 100.0%; Score 65; DB 5; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CDCRGDCFC 9
 Db 1 CDCRGDCFC 9
 RESULT 32
 AAE17983
 ID AAE17983 standard; peptide; 9 AA.
 XX
 XX AAE17983;
 AC
 XX 07-MAY-2002 (first entry)
 DT
 XX Human ligand #3 attached to an adenoviral vector.
 DE
 XX Human; adenoviral coat protein; non-native ligand; cell-surface receptor;
 KW therapy; anti-tumour agent; tumour necrosis factor; cancer; brain; lung;
 KW ovary; breast; prostate; alphavbeta3 integrin.
 XX
 XX Homo sapiens.
 OS

XX WO200192549-A2.
XX
XX
XX PD 06-DEC-2001.
XX
XX PF 30-MAY-2001; 2001WO-US017391.
XX
XX PR 31-MAY-2000; 2000US-0208451P.
XX PR 02-AUG-2000; 2000US-00631191.
XX
XX PA (GENV-) GENVEC INC.
XX
XX PI Wickham TJ, Kovesdi I, Roelvink PW, Einfeld D, Brough DE;
XX PI Lizonova A;
XX
XX DR WPI; 2002-147620/19.
XX
XX PT Adenoviral coat protein which permits production of adenoviral vectors
XX PT that bind and infect host cells not naturally infected by adenovirus,
XX PT comprises various non-native ligands.
XX PS Claim 4; Page 40; 45pp; English.
XX
XX CC The invention relates to adenoviral coat proteins comprising various non-
XX CC native ligands. The invention provides a method of controlled gene
XX CC expression utilising selectively replication competence and also a method
XX CC and a composition for targeting an adenoviral vector. A system
XX CC comprising a cell having a non-native cell-surface receptor, and a virus
XX CC having a non-native ligand which binds the non-native cell-surface
XX CC receptor of the cell is useful for propagating a virus and also for
XX CC assaying gene function. The system is also useful for isolating a nucleic
XX CC acid encoding a product comprising a desired property. Further the system
XX CC is useful for identifying functionally related coding sequences.
XX CC Adenoviral vector comprising a non-native nucleic acid encoding a
XX CC therapeutic agent such as anti-tumour agent, preferably tumour necrosis
XX CC factor and a second non-native nucleic acid encoding an agent that
XX CC facilitates imaging and a targeting agent is useful for treating an
XX CC animal. The therapeutic agent can be used to treat cancer of the brain,
XX CC lung, ovary, breast and prostate. The present sequence is human non-
XX CC native ligand specific for alphavbeta3 integrin, attached to an
XX CC adenoviral vector
XX
XX SQ Sequence 9 AA;

Query Match 100.0%; Score 65; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDCRGDCFC 9
Db 1 CDCRGDCFC 9

RESULT 33
ABE78354
ID ABE78354 standard; peptide; 9 AA.
XX
XX AC ABE78354;
XX
XX DT 16-DEC-2002 (first entry)
XX
XX DE Amino acid sequence of a peptide ligand.
XX
XX KW Tetraether lipid derivative; liposome; lipid aggregate;
XX KW in vitro transfection; gene therapy; packaging; peptide ligand; circular.
XX
XX OS Unidentified.
XX
XX PN DE10065561-A1.
XX
XX PD 11-JUL-2002.
XX
XX PF 28-DEC-2000; 2000DE-01065561.

XX
XX PR 28-DEC-2000; 2000DE-01065561.
XX
XX PA (BERN-) BERNINA BIOSYSTEMS GMBH.
XX
XX PI Kuehl C, Tewes B, Hagen M, Gropp F, Littger R, Marx U;
XX
XX XX WPI; 2002-675953/73.
XX
XX DR New tetraether lipid derivative, useful e.g. for preparing liposomes and
XX PT lipid aggregates for gene therapy or in vitro transfection.
XX
XX PS Disclosure; Page 12; 44pp; German.
XX
XX CC The invention describes tetraether lipid derivatives, of a formula given
XX CC in the specification. Liposomes, or lipid aggregates, that contain one or
XX CC more of these lipid derivatives are useful for in vitro transfection of
XX CC eukaryotic cells; for gene therapy and for packaging active ingredients
XX CC for oral, (parenteral or topical delivery. The lipid derivatives are
XX CC also used to coat surfaces, e.g. of metal or plastic, such as stents and
XX CC implants, and, where the resulting monolayers also include hydrophobic
XX CC active ingredients, these may be released gradually, e.g. to improve
XX CC compatibility. The present sequence represents a peptide ligand, which is
XX CC circularised by a disulphide bond
XX
XX SQ Sequence 9 AA;

Query Match 100.0%; Score 65; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDCRGDCFC 9
Db 1 CDCRGDCFC 9

RESULT 34
ABG70754
ID ABG70754 standard; peptide; 9 AA.
XX
XX AC ABG70754;
XX
XX DT 28-NOV-2002 (first entry)
XX
XX DE Targeting moiety peptide motif #1.
XX
XX KW Diagnostic; negatively charged carrier; targeting moiety; tumour;
XX KW endothelial tumour; microbiological organism; cyclic.
XX
XX OS Synthetic.
XX
XX PN EP1209469-A1.
XX
XX PD 29-MAY-2002.
XX
XX PF 22-NOV-2001; 2001EP-00127384.
XX
XX PR 22-NOV-2000; 2000US-0252666P.
XX
XX PA (VECT-) VECTRON THERAPEUTICS AG.
XX
XX PI Brueselbach S, Fahr A, Graser A;
XX
XX DR WPI; 2002-683934/74.
XX
XX PT Diagnostic system for diagnosing e.g. tumors has a carrier, targeting
XX PT moiety and diagnostic agent.
XX
XX PS Example 8; Page 10; 30pp; English.
XX
XX CC The invention discloses a diagnostic system comprising at least one
XX CC negatively charged carrier, a targeting moiety and a diagnostic agent.
XX CC The diagnostic kit comprises at least one negatively charged carrier and

CC diagnostic agent. The system is useful for diagnosis of disease e.g.
 CC tumours, particularly endothelial tumours and for in vivo diagnosis (in
 CC cells and tissues) and diagnosis of microbiological organisms in vitro.
 CC The system improves the persistence of the diagnostic agent in the cell
 CC or tissue, has a long shelf life and a low toxicity. The sequence
 CC presented is the targeting moiety peptide motif #1
 XX
 XX Sequence 9 AA;
 SQ
 Query Match 100.0%; Score 65; DB 5; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CDCRGDCFC 9
 |||||
 Db 1 CDCRGDCFC 9
 RESULT 35
 AAU75609
 ID AAU75609 standard; peptide; 9 AA.
 XX
 AC AAU75609;
 XX
 DT 08-MAY-2002 (first entry)
 XX
 DE Synthetic peptide used in binding assay of Tumstatin-45-132.
 XX
 KW Human; type IV collagen alpha 3 chain; cytostatic; antiangiogenic;
 KW non-Goodpasture fragment; alpha3(IV)NC1 domain; alphavbeta3 integrin;
 KW endothelial cell proliferation; apoptosis; Arresten; Canstatin;
 KW Tumstatin; angiogenesis; tumour.
 XX
 OS Synthetic.
 XX
 FN WO200151523-A2.
 XX
 PD 19-JUL-2001.
 XX
 PF 08-JAN-2001; 2001WO-US000565.
 XX
 PR 07-JAN-2000; 2000US-00479118.
 PR 04-APR-2000; 2000US-00543371.
 PR 21-JUL-2000; 2000US-00625191.
 XX
 XX (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
 FA
 XX Kalluri R;
 PI
 XX WPI; 2002-188037/24.
 DR
 XX
 XX A non-Goodpasture fragment of alpha3(IV)NC1 domain used in detecting and
 PT treating disorders involving angiogenesis.
 PT
 XX Example 45; Page 143; 205pp; English.
 PS
 XX The invention relates to a non-Goodpasture fragment of alpha3(IV)NC1
 CC domain, having one or more of the characteristics selected from: (a) the
 CC ability to bind alphavbeta3 integrin; (b) the ability to inhibit
 CC proliferation of endothelial cells; and (c) the ability to cause
 CC apoptosis of endothelial cells. Also described are the following: (1) use
 CC of Arresten, Canstatin or Tumstatin, or a fragment, mutant, homologue,
 CC analogue or allelic variant in the preparation of a medicament for
 CC treating a disorder involving: (a) inhibiting angiogenesis in a tissue,
 CC where the angiogenesis is mediated by one or more endothelial cell
 CC integrins or one or more endothelial cell integrin subunits; or (b) by
 CC promoting or inducing endothelial cell apoptosis in a tissue, where the
 CC endothelial cell apoptosis is mediated by one or more endothelial cell
 CC integrins or one or more endothelial cell integrin subunits; (2) use of
 CC an antibody or peptide that specifically binds the alpha1, alpha2,
 CC alpha3, alpha5, alpha6, alpha7, beta1 or beta3 subunit of integrin in the
 CC preparation of a medicament for inhibiting angiogenesis or cell
 CC proliferation; (3) use of an inhibitor, such as an antibody, antibody

CC fragment or peptide of receptor-mediated angiogenesis in the preparation
 CC of a medicament for treating a proliferative disease in a vertebrate,
 CC where the disease is characterised by angiogenesis that is mediated by
 CC receptors to Arresten, Canstatin or Tumstatin and where the receptors
 CC inhibited are Arresten, Canstatin or Tumstatin receptors; (4) use of one
 CC or more soluble receptors that bind Arresten, Canstatin or Tumstatin in
 CC the presence of a medicament for promoting angiogenesis in a tissue; and
 CC (5) use of integrins in the preparation of a medicament for promoting or
 CC inducing angiogenesis or cell proliferation in a tissue. The fragments
 CC Arresten, Canstatin or Tumstatin and their mutants, homologues, analogues
 CC or allelic variants are useful in the preparation of a medicament for
 CC treating a disorder involving inhibiting angiogenesis in a tissue, where
 CC the angiogenesis is mediated by one or more endothelial cell integrins or
 CC one or more endothelial cell integrin subunits; or by promoting or
 CC inducing endothelial cell apoptosis in a tissue, where the endothelial
 CC cell apoptosis is mediated by one or more endothelial cell integrins or
 CC one or more endothelial cell integrin subunits. The medicament is useful
 CC in inhibiting tumour growth and for the regression of an established
 CC tumour. The present sequence represents a synthetic peptide used in a
 CC binding assay of human type IV collagen alpha 3 chain mutant, Tumstatin-
 CC 45-132
 XX
 XX Sequence 9 AA;
 SQ

Query Match 100.0%; Score 65; DB 5; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDCRGDCFC 9
 |||||
 Db 1 CDCRGDCFC 9

RESULT 36

AAU79138
 ID AAU79138 standard; peptide; 9 AA.

XX
 AC AAU79138;

XX
 DT 18-JUN-2002 (first entry)

XX
 DE Synthetic peptide #38 used for production of cancer treating kit.

XX
 DE Cyclic; cytostatic; tumour neovascular; receptor; binder; cancer;

XX
 KW anticancer agent; radiosensitizer agent; photodynamic therapy;

XX
 KW tumour imaging; angiogenesis; rheumatoid arthritis; kit; alpha-v-beta3;

XX
 KW alpha-v-beta5.

XX
 OS Synthetic.

XX
 FN WO200197860-A2.

XX
 PD 27-DEC-2001.

XX
 PF 21-JUN-2001; 2001WO-US020108.

XX
 PR 21-JUN-2000; 2000US-0213206P.

XX
 PA (DUPO) DUPONT PHARM CO.

PI Rajopadhye M, Edwards DS, Barrett JA, Carpenter AP, Heminway SJ;

PI Liu S, Singh P;

XX
 WPI; 2002-195659/25.

XX
 PT Kit used for treating cancer comprises peptide compound and anticancer
 PT and/or radiosensitizer agent.

XX
 PS Disclosure; Page 106; 306pp; English.

XX
 CC The present invention relates to a new kit which comprises a peptide
 CC compound, an anticancer agent and/or radiosensitizer agent and a carrier.
 CC The kit of the invention can be used for treating cancer, preferably in

CC combination with photodynamic therapy, for tumour imaging and for
 CC monitoring the progress and results of therapeutic angiogenesis
 CC treatment. The invention is also used for treating rheumatoid arthritis.
 CC The present amino acid sequence represents one of a collection of
 CC peptides (AAU79101-AAU79139) used in the methods of the invention for the
 CC production of kits used for treating cancer. The present sequence binds
 CC alpha-v-beta3 and alpha-v-beta5
 XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 65; DB 5; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDCRGDCFC 9
 Db 1 CDCRGDCFC 9

RESULT 37
 AAU98972
 ID AAU98972 standard; peptide; 9 AA.

XX
 AC AAU98972;

XX
 DT 05-NOV-2002 (first entry)

XX
 DE Adeno-associated virus (AAV) targeting peptide #1.

XX
 KW Adeno-associated virus 2 vector; AAV2; cancer; VPI capsid;
 KW heparin-sulphate proteoglycan; vaccine; immune response; ovarian cancer;
 KW cyclic.

XX
 OS Synthetic.

XX
 PN WO200253703-A2.

XX
 PD 11-JUL-2002.

XX
 PF 04-JAN-2002; 2002WO-US0000152.

XX
 PR 05-JAN-2001; 2001US-0260124P.

XX
 PA (CHIL-) CHILDRENS HOSPITAL INC.

XX
 PI Bartlett JS;

XX
 PS WPI; 2002-583608/62.

XX
 PT New adeno-associated virus vector comprises a biotinylated capsid or
 PT capsid protein with an amino acid insertion in the VPI capsid, useful as
 PT a vaccine or for transferring a therapeutic peptide to a cancer cell.

XX
 PS Claim 10; Page 38; 57pp; English.

XX
 CC The invention relates to an adeno-associated virus (AAV) vector (I)
 CC comprising a biotinylated capsid or capsid protein (II) with an amino
 CC acid insertion following the capsid amino acid at position 139, 161, 588
 CC or 657 in the VPI capsid. The AAV vector comprises a capsid protein
 CC containing one or more amino acid insertions that ablate the ability of
 CC the vector to bind heparin-sulphate proteoglycan and allow the vector to
 CC use a cellular receptor not used by wild type AAV. Modified (I) are
 CC useful as vaccines to elicit immune responses to amino acids, where the
 CC response can be protective and/or therapeutic. (I) may be used to
 CC transfer a therapeutic peptide to a cancer cell, particularly to an
 CC ovarian cancer cell. The present sequence represents an AAV targeting
 CC peptide used to make mutant AAV vectors of the invention
 XX

SQ Sequence 9 AA;

Query Match 100.0%; Score 65; DB 5; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDCRGDCFC 9
 Db 1 CDCRGDCFC 9

RESULT 38
 AAM48795
 ID AAM48795 standard; peptide; 9 AA.

XX
 AC AAM48795;

XX
 DT 08-APR-2002 (first entry)

XX
 DE Tumour-targeting peptide vector peptide SEQ ID NO 1.

XX
 KW Tumour; integrin; histidinated polylysine; cytostatic; peptide targeting;
 KW cancer.

XX
 OS Synthetic.

XX
 PN JP2001309790-A.

XX
 PD 06-NOV-2001.

XX
 PF 02-MAY-2000; 2000JP-00134059.

XX
 PR 02-MAY-2000; 2000JP-00134059.

XX
 PA (KAGA-) KAGAKU GIUTSU SHINKO JIGYODAN.

XX
 DR WPI; 2002-134852/18.

XX
 PT Tumour-targeting peptide vector for diagnosing and treating progressive
 PT solid cancer, comprises a peptide having a ligand motif of integrin and a
 PT peptide having histidinated polylysine.

XX
 PS Disclosure; Page 4; 8pp; Japanese.

XX
 CC The invention relates to a tumour-targeting peptide vector comprising a
 CC peptide containing a ligand motif of integrin combined with a peptide
 CC consisting of histidinated polylysine and where the histidinated
 CC polylysine has 20 to 40 lysine residues and one histidine is added to 4
 CC lysine residues. The peptide vector has cytostatic activity and can be
 CC used for the treatment of progressive solid cancer patients and the
 CC diagnosis of progressive solid cancers. The present sequence is that of a
 CC peptide of the invention
 XX

SQ Sequence 9 AA;

Query Match 100.0%; Score 65; DB 5; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDCRGDCFC 9
 Db 1 CDCRGDCFC 9

RESULT 39
 ABB79525
 ID ABB79525 standard; peptide; 9 AA.

XX
 AC ABB79525;

XX
 DT 23-SEP-2002 (first entry)

XX
 DE RGD motif-containing peptide.

XX
 KW RGD motif; integrin; tumour; metastasis; imaging.

XX
 OS Unidentified.

PA (DUPO) DUPONT PHARM CO.
 XX
 PI Liu S;
 XX
 DR WPI; 2002-049126/06.
 XX
 PT New macrocyclic chelants, useful for treating cancer, diagnosing
 PT thromboembolic disorders, atherosclerosis, infection, inflammation and
 PT transplant rejection, detecting new angiogenic vasculature and metal
 PT detoxification.
 XX
 PS Disclosure; Page 84; 136pp; English.
 XX
 CC This invention relates to macrocyclic chelants and their salts. They are
 CC useful in compositions for treating cancer, diagnosing thromboembolic
 CC disorders, atherosclerosis, infections, inflammation and transplant
 CC rejection, and for detecting new angiogenic vasculature and metal
 CC detoxification. This peptide sequence represents a cyclic peptide that
 CC binds to alpha-V-beta-3 and alpha-V-beta-5
 XX
 SQ Sequence 9 AA;
 XX
 Query Match 100.0%; Score 65; DB 5; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CDCRGDCFC 9
 Db |||||
 1 CDCRGDCFC 9
 RESULT 42
 AAM51995
 ID AAM51995 standard; peptide; 9 AA.
 XX
 AC AAM51995;
 XX
 DT 12-FEB-2002 (first entry)
 XX
 DE Drug targeting peptide RGD-4C.
 XX
 KW Targeting vector; angiogenesis associated receptor; integrin receptor;
 KW alphavbeta3; cancer; heart disease; atherosclerosis; inflammation;
 KW rheumatoid arthritis; gingivitis; osteoarthritis; psoriasis; cytostatic;
 KW antiinflammatory; antiarteriosclerotic; antirheumatic; antiarthritic;
 KW anti-HIV; osteopathic; antipsoriatic; antidiabetic; ophthalmological;
 KW dermatological; antiulcer; ulcerative colitis.
 XX
 OS Synthetic.
 XX
 PN WO200177145-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-N0000146.
 XX
 PR 12-APR-2000; 2000GB-00009042.
 PR 12-OCT-2000; 2000GB-00025070.
 XX
 PA (NYCO-) NYCOMED IMAGING AS.
 XX
 PI Cuthbertson A, Indrevoll B;
 XX
 DR WPI; 2002-049128/06.
 XX
 CC New peptide-based compounds useful as a diagnostic imaging agent
 PT comprises affinity for integrin receptors.
 XX
 PS Disclosure; Page 5; 63pp; English.
 XX
 CC The present invention relates to peptide-based compounds which have
 CC affinity for integrin receptors, particularly the integrin alphavbeta3
 CC receptor. These can be used in the manufacture of a contrast medium for

CC use as a diagnostic imaging agent for generating images of a human or non
 CC -human animal for treating cancer or a related disease, and as targeting
 CC vectors that bind to receptors associated with angiogenesis. Diseases and
 CC indications associated with angiogenesis include arteriovenous
 CC malformations, astrocytomas, choriocarcinomas, glioblastomas, gliomas,
 CC hemangiomas (childhood capillary), hepatomas, hyperplastic endometrium,
 CC ischaemic myocardium, Kaposi sarcoma, macular degeneration, melanoma,
 CC neuroblastomas, occluding peripheral artery disease, osteoarthritis,
 CC psoriasis, retinopathy (diabetic, proliferative), scleroderma, seminomas,
 CC rheumatoid arthritis, atherosclerosis, inflammation, gingivitis and
 CC ulcerative colitis. The present sequence is a peptide which can be used
 CC in a compound of the invention
 XX
 SQ Sequence 9 AA;
 XX
 Query Match 100.0%; Score 65; DB 5; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CDCRGDCFC 9
 Db |||||
 1 CDCRGDCFC 9
 RESULT 43
 ABG73024
 ID ABG73024 standard; peptide; 9 AA.
 XX
 AC ABG73024;
 XX
 DT 28-FEB-2003 (first entry)
 XX
 DE Integrin AlphasBeta3 subunit antagonist #4.
 XX
 KW Vitronectin receptor; cardiac perfusion; imaging agent;
 KW perfusion imaging agent; tricine; TPPTS; angiogenesis; organ perfusion;
 KW tris(3-sulphonatophenyl)phosphine trisodium salt; vulnerable plaque;
 KW perfusion abnormality; endothelial damage; cancer; brain perfusion;
 KW integrin AlphasBeta3 subunit; antagonist.
 XX
 OS Synthetic.
 XX
 PN US2002106325-A1.
 XX
 PD 08-AUG-2002.
 XX
 PF 27-NOV-2001; 2001US-00995388.
 XX
 PR 27-NOV-2000; 2000PH-00007201.
 XX
 PA (CARP/) CARPENTER A P.
 XX
 PI Carpenter AP;
 XX
 DR WPI; 2003-057227/05.
 XX
 PT Simultaneous imaging using vitronectin receptor targeted and perfusion
 PT imaging agent, useful for imaging sites of angiogenesis, organ perfusion,
 PT endothelial damage, site of vulnerable plaque and perfusion
 PT abnormalities.
 XX
 PS Disclosure; Page 21; 86pp; English.
 XX
 CC The invention relates to a method of concurrent imaging involving
 CC administration of a vitronectin receptor targeted imaging agent and a
 CC perfusion imaging agent, detection of both agents and formation of a
 CC combined image. Also included is a kit comprising: (i) a compound (I) or
 CC (II) where the compound comprises: (1) a chelator capable of chelating
 CC the metal; (2) a targeting moiety where the targeting moiety is bound to
 CC the chelator, and (3) 0-1 linking groups between the targeting moiety and
 CC the chelator, and where the targeting moiety is a peptide or
 CC peptidomimetic which binds to a vitronectin receptor; (ii) a reducing
 CC agent (preferably tin (II)); (iii) one or more ancillary ligands

CC (preferably tricine or tris(3-sulphonatophenyl)phosphine trisodium salt
 CC (TPPSS). The method is for use in concurrent imaging sites of
 CC angiogenesis, organ perfusion, in diagnosing and localising sites of
 CC localisation of sites of vulnerable plaque and perfusion abnormalities,
 CC and of endothelial damage. The method is also useful for diagnosis and
 CC treatment of cancer. The perfusion imaging agents include cardiac and
 CC brain perfusion agents. The combination of a vitronectin targeted imaging
 CC agent and the perfusion imaging agent provide additive or synergistic
 CC therapeutic response without unacceptable additive toxicity. There is
 CC also a much lower systemic radiation exposure to the patient. The present
 CC sequence is an integrin Alpha5Beta3 subunit antagonist included in the
 CC specification
 XX
 XX SQ Sequence 9 AA;

Query Match 100.0%; Score 65; DB 6; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDCRGDCFC 9
 Db 1 CDCRGDCFC 9

RESULT 44
 ABB84641
 ID ABB84641 standard; peptide; 9 AA.

XX AC ABB84641;

XX DT 05-FEB-2003 (first entry)

XX DE Human integrin peptide SEQ ID 1.

XX KW Integrin; human; image enhancing agent; selectin; bioluminescence image;
 XX matrix metalloproteinase; MMP; chondroitin sulphate proteoglycan;
 XX computer assisted tomography; CAT; magnetic resonance spectroscopy; MRS;
 XX magnetic resonance imaging; MRI; positron emission tomography; PET;
 XX single-photon emission computed tomography; SPPECT; BLI;
 XX tumour neovasculation; anti-tumour; cell growth disorder; cancer.

XX OS Homo sapiens.

XX PN US2002122806-A1.

XX PD 05-SEP-2002.

XX PF 05-MAR-2001; 2001US-00734628.

XX PR 05-MAR-2001; 2001US-00734628.

XX PA (CHIN/) CHINNAIAN A M.

XX PA (REHE/) REHEMULLA A.

XX PA (ROSS/) ROSS B D.

XX PI Chinnaian AM, Rehemulla A, Ross BD;

XX DR WPI; 2003-066773/06.

XX PT Novel chimeric molecule for imaging sites of primary/metastatic tumors
 XX and tumor neovasculation, comprises first domain having e.g. fluorescent
 XX polypeptide and second domain having e.g. selectin-binding polypeptide.

XX PS Claim 9; Page 10; 15pp; English.

XX CC This invention describes a novel chimeric molecule comprising a first
 CC domain having an image enhancing agent e.g. a fluorescent, bioluminescent
 CC or chemiluminescent polypeptide, or a heterologous kinase, and a second
 CC domain comprising RGD motif-comprising polypeptide, selectin-binding
 CC polypeptide, matrix metalloproteinase (MMP)-binding polypeptide or
 CC chondroitin sulphate proteoglycan-binding polypeptide. The molecule of
 CC the invention can be used in a pharmaceutical formulation capable of

CC binding to a cell, a tissue or an organ in a cell-, tissue- or organ-
 CC specific manner, which enhances a computer assisted tomography (CAT)
 CC image, a magnetic resonance spectroscopy (MRS) image, a magnetic
 CC resonance imaging (MRI) image, a positron emission tomography (PET)
 CC image, a single-photon emission computed tomography (SPPECT) image or a
 CC bioluminescence image (BLI). The formulation can be used for in situ or
 CC in vivo imaging of a cell, tissue (tumour tissue) or organ or a full
 CC body, useful for in vivo imaging of tumour neovasculation in an
 CC individual and for in vivo screening of anti-tumour agents. The product
 CC of the invention is useful for non-invasively evaluating the
 CC effectiveness of therapy for disorders of cell growth, such as cancer.
 CC This sequence represents a human integrin-derived peptide used to
 CC illustrate the method of the invention
 XX
 XX SQ Sequence 9 AA;

Query Match 100.0%; Score 65; DB 6; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDCRGDCFC 9
 Db 1 CDCRGDCFC 9

RESULT 45

ABU59556

ID ABU59556 standard; peptide; 9 AA.

XX AC ABU59556;

XX DT 22-APR-2003 (first entry)

XX DE Tumour angiogenic epithelium-targeting peptide #1.

XX KW Targeting ligand; bioactive agent; polymer matrix; cancer; cytostatic;
 XX cathepsin-D substrate; peptides; neuroreceptor; adrenal receptor;
 XX fibronectin; vitronectin; integrin; RGD motif; angiogenic endothelium;
 XX tumour; cationic cancer-targeting peptide.

XX OS Synthetic.

XX PN US2002041898-A1.

XX PD 11-APR-2002.

XX PF 25-JUL-2001; 2001US-00912609.

XX PR 05-JAN-2000; 2000US-00478124.

XX PR 31-OCT-2000; 2000US-00703474.

XX PA (UNGE/) UNGER E C.

XX PA (MATS/) MATSUNAGA T O.

XX PA (RAMA/) RAMASWAMI V.

XX PA (ROMA/) ROMANOWSKI M J.

XX PI Unger EC, Matsunaga TO, Ramaswami V, Romanowski MJ;

XX DR WPI; 2003-208921/20.

XX PT Targeted delivery system comprising a bioactive agent homogeneously
 XX dispersed in a targeted matrix is especially useful in cancer therapy.

XX PS Claim 46; Page 38; 46pp; English.

XX CC The invention relates to a composition comprising a bioactive agent
 CC homogeneously dispersed in a targeted matrix (polymer and targeting
 CC ligand). Also included are a targeted matrix for use as a delivery
 CC vehicle comprising a polymer associated with a targeting ligand,
 CC enhancing the bioavailability of an agent comprising administration of
 CC the composition and treating cancer comprising administration of the
 CC novel composition. The method is useful for targeted delivery of a drug,
 CC especially in cancer therapy. The targeting ligand may be a peptide.

CC Examples of targeting peptides are disclosed including cathelin-D
 CC substrate peptides, peptides targeting receptors in the brain and kidney,
 CC peptides recognising fibronectin- and vitronectin-binding integrins,
 CC peptides targeting the RGD (Arg-Gly-Asp)-motif in, e.g., antibodies,
 CC peptides targeting the angiogenic endothelium of solid tumours, tissue
 CC specific peptides (e.g. of lung, skin, pancreas, intestine, uterus,
 CC adrenal gland and retina), and cationic cancer-targeting peptides. The
 CC present sequence is a peptide targeting ligand disclosed in the invention
 XX
 SQ Sequence 9 AA;
 Query Match 100.0%; Score 65; DB 6; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CDCRGDCFC 9
 DB 1 CDCRGDCFC 9
 RESULT 46
 ABU08571
 ID ABU08571 standard; peptide; 9 AA.
 XX
 AC ABU08571;
 XX
 DT 05-JUN-2003 (first entry)
 XX
 DE RGD-containing, tumour targeting peptide #1.
 XX
 KW TNF related apoptosis inducing ligand; TRAIL; integrin;
 KW tumour necrosis factor; apoptosis; haemostatic; immunosuppressive;
 KW antiinflammatory; dermatological; thrombotic microangiopathy;
 KW thrombotic thrombocytopenic purpura; TTP; HUS; SLE; clotting disorder;
 KW adult haemolytic uraemic syndrome; cardiac problem; paediatric AIDS;
 KW systemic lupus erythematosus; tumour targeting peptide.
 XX
 OS Unidentified.
 XX
 PN US6521228-B1.
 XX
 PD 18-FEB-2003.
 XX
 PF 02-APR-2001; 2001US-00825563.
 XX
 PR 29-JUN-1995; 95US-00496632.
 PR 01-NOV-1995; 95US-00548368.
 PR 25-JUN-1996; 96US-00670354.
 PR 26-MAR-1998; 98US-00048641.
 PR 10-NOV-1998; 98US-00190046.
 PR 26-MAY-1999; 99US-00320424.
 XX
 PA (IMMV) IMMUNEX CORP.
 XX
 PI Wiley SR, Goodwin RG;
 XX
 WPI; 2003-340628/32.
 XX
 PT Novel antibody which binds to human tumor necrosis factor related
 PT apoptosis inducing ligand protein, useful for inhibiting TRAIL-mediated
 PT apoptosis of a target cell, or blocking binding of TRAIL to a target
 PT cell.
 XX
 PS Disclosure; Col 11; 40pp; English.
 XX
 CC The invention relates to an antibody that specifically binds: (a) the
 CC human tumor necrosis factor (TNF) related apoptosis inducing ligand
 CC (TRAIL) protein appearing as ABU08558; (b) a soluble human TRAIL
 CC polypeptide; (c) a polypeptide comprising amino acids 124-276 of
 CC ABU08558; or (d) a fragment of the TRAIL protein. Also included is an
 CC antigen-binding fragment of the antibody (a monoclonal antibody), a
 CC hybridoma cell line that produces the antibody. The antibody is used in
 CC assays to detect the presence of TRAIL polypeptides, either in vitro or

CC in vivo, purifying TRAIL by affinity chromatography, blocking binding of
 CC TRAIL to target cells and thus inhibiting a biological activity of TRAIL.
 CC The antibody is useful for treating disorders mediated or exacerbated by
 CC TRAIL, e.g. thrombotic microangiopathies, e.g. thrombotic
 CC thrombocytopenic purpura (TTP), adult haemolytic uraemic syndrome (HUS)
 CC (even though it can strike children as well) small blood vessel clotting
 CC disorders e.g., cardiac problems in paediatric AIDS patients and systemic
 CC lupus erythematosus (SLE). The present sequence is an RGD (Arg-Gly-Asp)
 CC containing, tumour targeting, peptide which is used in fusion proteins
 CC with TRAIL to allow the fusion protein to bind to alpha integrins
 XX
 SQ Sequence 9 AA;
 Query Match 100.0%; Score 65; DB 6; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CDCRGDCFC 9
 DB 1 CDCRGDCFC 9
 RESULT 47
 ABP60343
 ID ABP60343 standard; peptide; 9 AA.
 XX
 AC ABP60343;
 XX
 DT 20-FEB-2003 (first entry)
 XX
 DE Tumour vasculature integrin alpha-v-beta-3 or 5 targeting peptide 8.
 XX
 KW Radiopharmaceutical; ascorbic acid; tumour; vasculature;
 KW integrin alpha-v-beta-3.
 XX
 OS Synthetic.
 XX
 PN US2002122769-A1.
 XX
 PD 05-SRP-2002.
 XX
 PF 22-FEB-2002; 2002US-00081258.
 XX
 PR 26-FEB-2001; 2001US-0271389P.
 XX
 PA (LIUS/) LIU S.
 XX
 PI Liu S;
 XX
 WPI; 2003-119656/11.
 XX
 PT Buffering, chelating and stabilizing radiopharmaceutical involves
 PT targeting radiopharmaceutical with ascorbic acid analogs.
 XX
 PS Disclosure; Page 10; 21pp; English.
 XX
 CC The invention relates to buffering, chelating and stabilising a
 CC radiopharmaceutical by contacting the radiopharmaceutical with ascorbic
 CC acid analogues. The invention also includes a radiopharmaceutical
 CC composition comprising a radiolabelled chelator-biomolecule conjugate of
 CC formula M-Ch-Ln-(BM)_m, where: M = metallic isotope; Ch = metal chelator;
 CC Ln = optional linking group; BM = biomolecule; and m = 1-10. The present
 CC sequence is that of a tumour vasculature integrin alpha-v-beta-3 or 5
 CC targeting peptide, which can be included as the BM part of the
 CC radiopharmaceutical composition of the invention
 XX
 SQ Sequence 9 AA;
 Query Match 100.0%; Score 65; DB 6; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CDCRGDCFC 9

ID	ADC44955 standard; peptide; 9 AA.
XX	ADC44955;
AC	ADCA4955;
DT	18-DEC-2003 (first entry)
DE	Endothelial cell binding associated control peptide SEQ ID NO:685.
XX	Endothelial cell binding protein; EGBP; anti-tumour; cytostatic;
XX	endothelial cell binding protein; EGBP; anti-tumour; cytostatic;
KW	vasotrophic; antiproliferative; dermatological; ophthalmological;
KW	antidiabetic; antiarthritic; vulnerary; antitumor; antiinflammatory;
KW	antibacterial; gynaecological; angiogenesis.
XX	Synthetic.
OS	WO2003037172-A2.
XX	08-MAY-2003.
PD	01-NOV-2002; 2002WO-US035258.
PF	01-NOV-2001; 2001US-0334822P.
XX	(GPCB-) GPC BIOTECH INC.
PA	Gyuris J, Lamphere L, Morris AJ, Tsaion K;
PI	WPI; 2003-482072/45.
DR	Novel synthetic or recombinant polypeptide useful for promoting, reducing
XX	proliferation and/or migration of endothelial cells, and for modulating
PT	angiogenesis, has endothelial cell binding protein sequences.
PT	Disclosure; SEQ ID NO 685; 136pp; English.
PS	The invention relates to a novel isolated, synthetic or recombinant
CC	peptide or polypeptide which includes one or more endothelial cell
CC	binding protein (EGBP) sequences. A peptide of the invention has anti-
CC	tumour, cytostatic, vasotropic, antiproliferative, dermatological,
CC	ophthalmological, antidiabetic, antiarthritic, vulnerary, antitumor,
CC	antiinflammatory, antibacterial, and gynaecological activity. The peptide
CC	is useful for promoting, reducing the proliferation and/or migration of
CC	endothelial cells, by treating the cells with an EGBP agonist, which is
CC	preferably the peptide, to promote proliferation and/or migration of the
CC	treated cells, and for reducing or promoting angiogenesis, by treating
CC	the cells with an EGBP antagonist, which is preferably the peptide of the
CC	invention. A peptide of the invention is also useful for manufacturing a
CC	medicament for promoting angiogenesis, by administering an EGBP agonist or
CC	EGBP antagonist to promote or reduce angiogenesis at one or more sites in
CC	a treated mammal. The medicament is useful for promoting or reducing
CC	angiogenesis. EGBP sequences are useful to alter the infectivity spectrum
CC	of a viral particle. The present sequence represents an EGBP of the
CC	invention.
XX	Sequence 9 AA;
QY	Query Match 100.0%; Score 65; DB 7; Length 9;
DB	Best Local Similarity 100.0%; Pred. No. 1.4e+06;
DB	Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0
DB	1 CDCRGDCFC 9
DB	1 CDCRGDCFC 9
DB	Search completed: July 11, 2004, 10:08:50
DB	Job time : 52 secs

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OM protein - protein search, using sw model

Run on: July 11, 2004, 10:01:23 ; Search time 45 Seconds
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Title: US-09-734-628-1
Perfect score: 65
Sequence: 1 CDCRGDCFC 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

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6: /cgn2_6/ptodata/1/pubppa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubppa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubppa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubppa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubppa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubppa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubppa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubppa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubppa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubppa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubppa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/1/pubppa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubppa/US60_PUBCOMB.pep.*

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and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	65	100.0	9	9	US-09-765-086-1
2	65	100.0	9	9	US-09-845-160-5
3	65	100.0	9	9	US-09-245-603A-16
4	65	100.0	9	9	US-09-364-597A-16
5	65	100.0	9	9	US-09-734-628-1
6	65	100.0	9	9	US-09-971-798-5
7	65	100.0	9	9	US-09-969-192-3
8	65	100.0	9	9	US-09-840-277-38
9	65	100.0	9	9	US-09-840-277-62
10	65	100.0	9	10	US-09-801-485-2
11	65	100.0	9	10	US-09-791-524-124
12	65	100.0	9	12	US-10-609-217-450
13	65	100.0	9	12	US-10-609-217-1076
14	65	100.0	9	12	US-10-363-208-166
15	65	100.0	9	12	US-10-632-388-450

16	65	100.0	9	12	US-10-632-388-1076	Sequence 1076, Ap
17	65	100.0	9	12	US-10-652-244-20	Sequence 20, Appl
18	65	100.0	9	12	US-10-651-723-450	Sequence 450, App
19	65	100.0	9	12	US-10-651-723-1076	Sequence 1076, Ap
20	65	100.0	9	12	US-09-912-609-31	Sequence 31, Appl
21	65	100.0	9	12	US-09-995-388-47	Sequence 47, Appl
22	65	100.0	9	12	US-10-013-009-1	Sequence 1, Appl
23	65	100.0	9	12	US-10-033-769-10	Sequence 10, Appl
24	65	100.0	9	12	US-10-269-575-1	Sequence 1, Appl
25	65	100.0	9	12	US-10-645-761-450	Sequence 450, App
26	65	100.0	9	12	US-10-645-761-1076	Sequence 1076, Ap
27	65	100.0	9	13	US-10-080-854-8	Sequence 8, Appl
28	65	100.0	9	13	US-10-038-972A-10	Sequence 10, Appl
29	65	100.0	9	14	US-10-304-160-3	Sequence 3, Appl
30	65	100.0	9	14	US-10-264-374-1	Sequence 1, Appl
31	65	100.0	9	14	US-10-032-221B-35	Sequence 35, Appl
32	65	100.0	9	14	US-10-375-992-1	Sequence 1, Appl
33	65	100.0	9	16	US-10-666-696-450	Sequence 450, App
34	65	100.0	9	16	US-10-666-696-1076	Sequence 1076, Ap
35	65	100.0	9	16	US-10-653-048-450	Sequence 450, App
36	65	100.0	9	16	US-10-653-048-1076	Sequence 1076, Ap
37	65	100.0	9	16	US-10-264-374-1	Sequence 1, Appl
38	59	90.8	9	9	US-09-364-597A-17	Sequence 63, Appl
39	59	90.8	9	9	US-09-840-277-63	Sequence 451, App
40	59	90.8	9	12	US-10-609-217-451	Sequence 451, App
41	59	90.8	9	12	US-10-632-388-451	Sequence 451, App
42	59	90.8	9	12	US-10-651-723-451	Sequence 451, App
43	59	90.8	9	12	US-10-645-761-451	Sequence 451, App
44	59	90.8	9	16	US-10-666-696-451	Sequence 451, App
45	59	90.8	9	16	US-10-653-048-451	Sequence 451, App

ALIGNMENTS

RESULT 1

US-09-765-086-1
; Sequence 1, Application US/09765086
; Patent No. US20010046498A1
; GENERAL INFORMATION:
; APPLICANT: Ruuslahti, Erkki
; APPLICANT: Pasqualini, Renata
; APPLICANT: Wadit, Arap
; APPLICANT: Bredesen, Dale E.
; APPLICANT: Ellerby, H. Michael
; TITLE OF INVENTION: Chimeric Prostate-Homing Peptides With
; FILE REFERENCE: P-LJ 3844
; CURRENT APPLICATION NUMBER: US/09/765,086
; CURRENT FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US 09/489,582
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 235
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-09-765-086-1

Query Match 100.0%; Score 65; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDCRGDCFC 9

Db 1 CDCRGDCFC 9

RESULT 2

US-09-845-160-5

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; Sequence 5, Application US/09845160
; Patent No. US20020058045A1
; GENERAL INFORMATION:
; APPLICANT: MIZUGUCHI, HIROYUKI
; APPLICANT: HAYAKAWA, TAKAO
; TITLE OF INVENTION: ADENOVIRUS VECTOR
; FILE REFERENCE: 081356/0163
; CURRENT APPLICATION NUMBER: US/09/845,160
; CURRENT FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: JP 2001-131688
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: JP 2000-161577
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: RGD-4C peptide.
US-09-845-160-5

Query Match 100.0%; Score 65; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDCRGDCFC 9
DB 1 CDCRGDCFC 9

RESULT 3
US-09-245-603A-16
; Sequence 16, Application US/09245603A
; Patent No. US20020081280A1
; GENERAL INFORMATION:
; APPLICANT: Curiel, David T.
; APPLICANT: Krasnykh, Victor N.
; APPLICANT: Dmitriev, Igor
; TITLE OF INVENTION: Adenovirus Vector Containing A Heterologous Peptide
; TITLE OF INVENTION: Epitope in the HI Loop of the Fiber Knob
; FILE REFERENCE: D6080
; CURRENT APPLICATION NUMBER: US/09/245,603A
; CURRENT FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: US 60/099,801
; PRIOR FILING DATE: 1998-09-10
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 16
; LENGTH: 9
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of a RGD peptide incorporated
; OTHER INFORMATION: into the region of the fiber gene within the HI loop.
US-09-245-603A-16

Query Match 100.0%; Score 65; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDCRGDCFC 9
DB 1 CDCRGDCFC 9

RESULT 4
US-09-364-597A-16
; Sequence 16, Application US/09364597A
; Patent No. US20020103130A1
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Koivunen, Erkki
```

```
; TITLE OF INVENTION: No. US20020103130A1el Integrin-Binding Peptides
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/364,597A
; FILING DATE: 30-JUL-1999
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/158,001
; FILING DATE: 24-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/286,861
; FILING DATE: 04-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LA 3419
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (858) 535-9001
; TELEFAX: (858) 535-8949
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: circular
US-09-364-597A-16

Query Match 100.0%; Score 65; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDCRGDCFC 9
DB 1 CDCRGDCFC 9

RESULT 5
US-09-734-628-1
; Sequence 1, Application US/09734628
; Patent No. US20020122806A1
; GENERAL INFORMATION:
; APPLICANT: Chinnaiyan, Arul M.
; APPLICANT: Rehmetulla, Alnawaz
; APPLICANT: Ross, Brian D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IN SITU AND
; TITLE OF INVENTION: IN VIVO IMAGING OF CELLS AND TISSUES
; FILE REFERENCE: 11203-005001
; CURRENT APPLICATION NUMBER: US/09/734,628
; CURRENT FILING DATE: 2000-12-11
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-09-734-628-1

Query Match 100.0%; Score 65; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 CDCRGDCFC 9
Db 1 CDCRGDCFC 9

RESULT 6

US-09-971-798-5
; Sequence 5, Application US/09971798
; Patent No. US20020132769A1
; GENERAL INFORMATION:
; APPLICANT: NO. US20020132769A1artis AG
; TITLE OF INVENTION: Targeting molecules
; FILE REFERENCE: 4-31615/GTI
; CURRENT APPLICATION NUMBER: US/09/971,798
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-971-798-5

Query Match 100.0%; Score 65; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0;

Qy 1 CDCRGDCFC 9
Db 1 CDCRGDCFC 9

RESULT 7

US-09-969-192-3
; Sequence 3, Application US/09969192
; Patent No. US20020151027A1
; GENERAL INFORMATION:
; APPLICANT: WICKHAM, THOMAS J.
; ROELVINK, PETRUS W.
; KOVESDI, IMRE

TITLE OF INVENTION: TARGETING ADENOVIRUS WITH USE OF
CONSTRAINED PEPTIDE MOTIFS

NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza - 49th Floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/969,192
FILING DATE: 01-Oct-2001

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 9-455061
FILING DATE: 06-DEC-1999
APPLICATION NUMBER: US 9-130225
FILING DATE: 06-AUG-1998
APPLICATION NUMBER: US 8-701124
FILING DATE: 21-AUG-1996

ATTORNEY/AGENT INFORMATION:
NAME: Hefner, M. Daniel
REGISTRATION NUMBER: 41,826
REFERENCE/DOCKET NUMBER: 213564
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids

; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-969-192-3

Query Match 100.0%; Score 65; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0;

Qy 1 CDCRGDCFC 9
Db 1 CDCRGDCFC 9

RESULT 8

US-09-840-277-38
; Sequence 38, Application US/09840277
; Patent No. US20020168363A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: KOHNO, TADAHIKO
; APPLICANT: LACEY, DAVID LEE
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: INTEGRIN/ADHESION ANTAGONISTS
; FILE REFERENCE: A-688A
; CURRENT APPLICATION NUMBER: US/09/840,277
; CURRENT FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: 60/198,919
; PRIOR FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 60/201,394
; PRIOR FILING DATE: 2000-05-03
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Integrin antagonist peptide
US-09-840-277-38

Query Match 100.0%; Score 65; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0;

Qy 1 CDCRGDCFC 9
Db 1 CDCRGDCFC 9

RESULT 9

US-09-840-277-62
; Sequence 62, Application US/09840277
; Patent No. US20020168363A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: KOHNO, TADAHIKO
; APPLICANT: LACEY, DAVID LEE
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: INTEGRIN/ADHESION ANTAGONISTS
; FILE REFERENCE: A-688A
; CURRENT APPLICATION NUMBER: US/09/840,277
; CURRENT FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: 60/198,919
; PRIOR FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 60/201,394
; PRIOR FILING DATE: 2000-05-03
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 62
; LENGTH: 9

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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Integrin antagonist peptide
US-09-840-277-62

Query Match      100.0%; Score 65; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDCRGDCFC 9
Db 1 CDCRGDCFC 9

RESULT 10
US-09-801-485-2
; Sequence 2, Application US/09801485
; Publication No. US20030077818A1
; GENERAL INFORMATION:
; APPLICANT: Dickerson, Erin B.
; APPLICANT: Helfard, Stuart C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TARGETING INTERLEUKIN-12
; FILE REFERENCE: TO MALIGNANT ENDOTHELIUM
; CURRENT APPLICATION NUMBER: US/09/801,485
; CURRENT FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-801-485-2

Query Match      100.0%; Score 65; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDCRGDCFC 9
Db 1 CDCRGDCFC 9

RESULT 11
US-09-791-524-124
; Sequence 124, Application US/09791524
; Publication No. US20030143209A1
; GENERAL INFORMATION:
; APPLICANT: Aventis Pharmaceuticals Products Inc.
; TITLE OF INVENTION: Targeted Adenovirus Vectors For Delivery Of Heterologous Genes
; FILE REFERENCE: A3119A
; CURRENT APPLICATION NUMBER: US/09/791,524
; CURRENT FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/09828
; PRIOR FILING DATE: 1998-08-27
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 124
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Adenovirus
; OTHER INFORMATION: INTEGRIN-BINDING PEPTIDE
US-09-791-524-124

Query Match      100.0%; Score 65; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDCRGDCFC 9
Db 1 CDCRGDCFC 9

RESULT 12
US-10-609-217-450
; Sequence 450, Application US/10609217
; Publication No. US20040044188A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/609,217
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 450
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: INTEGRIN-BINDING PEPTIDE
US-10-609-217-450

Query Match      100.0%; Score 65; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDCRGDCFC 9
Db 1 CDCRGDCFC 9

RESULT 13
US-10-609-217-1076
; Sequence 1076, Application US/10609217
; Publication No. US20040044188A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/609,217
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1076
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: INTEGRIN-BINDING PEPTIDE
US-10-609-217-1076

Query Match      100.0%; Score 65; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDCRGDCFC 9
Db 1 CDCRGDCFC 9
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RESULT 14
US-10-363-208-166
; Sequence 166, Application US/10363208
; Publication No. US20040048243A1
; GENERAL INFORMATION:
; APPLICANT: Board of Regents, The University of Texas System
; TITLE OF INVENTION: Methods and Compositions for In Vitro Targeting
; FILE REFERENCE: 005774.P005PCT
; CURRENT APPLICATION NUMBER: US/10/363,208
; CURRENT FILING DATE: 2003-03-07
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 166
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; NAME/KEY: Peptide
; LOCATION: (1)..(9)
; OTHER INFORMATION: synthetic construct
US-10-363-208-166

Query Match 100.0%; Score 65; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDCRGDCFC 9
| | | | |
Db 1 CDCRGDCFC 9

RESULT 15
US-10-632-388-450
; Sequence 450, Application US/10632388
; Publication No. US20040053845A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/632,388
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 450
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: INTEGRIN-BINDING PEPTIDE
US-10-632-388-450

Query Match 100.0%; Score 65; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDCRGDCFC 9
| | | | |
Db 1 CDCRGDCFC 9

RESULT 16
US-10-632-388-1076
; Sequence 1076, Application US/10632388
; Publication No. US20040053845A1
; GENERAL INFORMATION:

; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/632,388
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1076
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: INTEGRIN-BINDING PEPTIDE
US-10-632-388-1076

Query Match 100.0%; Score 65; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDCRGDCFC 9
| | | | |
Db 1 CDCRGDCFC 9

RESULT 17
US-10-652-244-20
; Sequence 20, Application US/10652244
; Publication No. US20040052788A1
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; APPLICANT: Goodwin, Raymond G.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/10/652,244
; CURRENT FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: US/09/796,581
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/320,424
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: 09/190,046
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 09/048,641
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 08/670,354
; PRIOR FILING DATE: 1996-06-25
; PRIOR APPLICATION NUMBER: 08/548,368
; PRIOR FILING DATE: 1995-11-01
; PRIOR APPLICATION NUMBER: 08/496,632
; PRIOR FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: artificial
; OTHER INFORMATION: peptide
US-10-652-244-20

Query Match 100.0%; Score 65; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDCRGDCFC 9
| | | | |

Db 1 CDCRGDCFC 9

RESULT 18
US-10-651-723-450
; Sequence 450, Application US/10651723
; Publication No. US20040057953A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/651,723
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 450
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: INTEGRIN-BINDING PEPTIDE
US-10-651-723-450

Query Match 100.0%; Score 65; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDCRGDCFC 9
|||||
Db 1 CDCRGDCFC 9

RESULT 19
US-10-651-723-1076
; Sequence 1076, Application US/10651723
; Publication No. US20040057953A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/651,723
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1076
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: INTEGRIN-BINDING PEPTIDE
US-10-651-723-1076

Query Match 100.0%; Score 65; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDCRGDCFC 9
|||||
Db 1 CDCRGDCFC 9

RESULT 20
US-09-912-609-31
; Sequence 31, Application US/09912609
; Publication No. US20020041898A1
; GENERAL INFORMATION:
; APPLICANT: UNGER, EVAN C.
; APPLICANT: MATSUNAGA, TERRY ONICHI
; APPLICANT: RAMASWAMI, VARADARAJAN
; APPLICANT: ROMANOWSKI, MAREK J.
; TITLE OF INVENTION: NOVEL TARGETED DELIVERY SYSTEMS FOR BIOACTIVE AGENTS
; FILE REFERENCE: 5030-0001.24
; CURRENT APPLICATION NUMBER: US/09/912,609
; CURRENT FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 09/703,474
; PRIOR FILING DATE: 2000-10-31
; PRIOR APPLICATION NUMBER: 09/478,124
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-912-609-31

Query Match 100.0%; Score 65; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDCRGDCFC 9
|||||
Db 1 CDCRGDCFC 9

RESULT 21
US-09-995-388-47
; Sequence 47, Application US/09995388
; Publication No. US20020106325A1
; GENERAL INFORMATION:
; APPLICANT: Carpenter, Jr., Alan P.
; TITLE OF INVENTION: SIMULTANEOUS IMAGING OF CARDIAC PERFUSION AND A VITRONECTIN
; FILE REFERENCE: BMS-2201
; CURRENT APPLICATION NUMBER: US/09/995,388
; CURRENT FILING DATE: 2001-11-27
; PRIOR APPLICATION NUMBER: US 60/253,324
; PRIOR FILING DATE: 2000-11-27
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 47
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-09-995-388-47

Query Match 100.0%; Score 65; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDCRGDCFC 9
|||||
Db 1 CDCRGDCFC 9

RESULT 22
US-10-013-009-1

; Sequence 1, Application US/10013009
; Publication No. US20020086815A1
; GENERAL INFORMATION:
; APPLICANT: McMorris, Trevor C.
; APPLICANT: Kelner, Michael J.
; TITLE OF INVENTION: Antitumor agents
; FILE REFERENCE: 103.008US3
; CURRENT APPLICATION NUMBER: US/10/013,009
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: US 09/386,555
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: US 09/026,633
; PRIOR FILING DATE: 1998-02-20
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic amino acid sequence
US-10-013-009-1

Query Match 100.0%; Score 65; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDCRGDCFC 9
||| |||||
Db 1 CDCRGDCFC 9

RESULT 23
US-10-033-769-10
; Sequence 10, Application US/10033769
; Publication No. US20020094316A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Shuang
; TITLE OF INVENTION: POLYPODAL CHELANTS FOR METALLOPHARMACEUTICALS
; FILE REFERENCE: BMS-2204
; CURRENT APPLICATION NUMBER: US/10/033,769
; CURRENT FILING DATE: 2001-12-27
; PRIOR APPLICATION NUMBER: US 60/260,619
; PRIOR FILING DATE: 2001-01-09
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-033-769-10

Query Match 100.0%; Score 65; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDCRGDCFC 9
||| |||||
Db 1 CDCRGDCFC 9

RESULT 24
US-10-269-575-1
; Sequence 1, Application US/10269575
; Publication No. US20030204049A1
; GENERAL INFORMATION:
; APPLICANT: CUTHBERTSON, ALAN
; APPLICANT: INDREVOLL, BARD
; TITLE OF INVENTION: PEPTIDE-BASED COMPOUNDS
; FILE REFERENCE: NIDN-10433
; CURRENT APPLICATION NUMBER: US/10/269,575

; CURRENT FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: PCT/NO01/00146
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: GB 0009042.3
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: GB 0025070.4
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: illustrative
; OTHER INFORMATION: peptide
US-10-269-575-1

Query Match 100.0%; Score 65; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDCRGDCFC 9
||| |||||
Db 1 CDCRGDCFC 9

RESULT 25
US-10-645-761-450
; Sequence 450, Application US/10645761
; Publication No. US20040071712A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/645,761
; CURRENT FILING DATE: 2003-08-18
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 450
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: INTEGRIN-BINDING PEPTIDE
US-10-645-761-450

Query Match 100.0%; Score 65; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDCRGDCFC 9
||| |||||
Db 1 CDCRGDCFC 9

RESULT 26
US-10-645-761-1076
; Sequence 1076, Application US/10645761
; Publication No. US20040071712A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS

```
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/645,761
; CURRENT FILING DATE: 2003-08-18
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1076
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: INTEGRIN-BINDING PEPTIDE
US-10-645-761-1076

Query Match      100.0%; Score 65; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CDCRGDCFC 9
Db      1 CDCRGDCFC 9

RESULT 27
US-10-080-854-8
; Sequence 8, Application US/10080854
; Publication No. US20020172940A1
; GENERAL INFORMATION:
; APPLICANT: GYURIS, JENO
; APPLICANT: MORRIS, ARON J.
; TITLE OF INVENTION: METHODS AND REAGENTS FOR ISOLATING BIOLOGICALLY ACTIVE
; FILE REFERENCE: MIV-106.01
; CURRENT APPLICATION NUMBER: US/10/080,854
; CURRENT FILING DATE: 2002-02-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: RGD motif
US-10-080-854-8

Query Match      100.0%; Score 65; DB 13; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CDCRGDCFC 9
Db      1 CDCRGDCFC 9

RESULT 28
US-10-038-972A-10
; Sequence 10, Application US/10038972A
; Publication No. US20020192823A1
; GENERAL INFORMATION:
; APPLICANT: J. Bartlett
; TITLE OF INVENTION: AAV VECTORS AND METHODS
; FILE REFERENCE: 28335/36996US
; CURRENT APPLICATION NUMBER: US/10/038,972A
; CURRENT FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: US 60/260,124
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 4C-RGD Peptide
US-10-038-972A-10

Query Match      100.0%; Score 65; DB 13; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CDCRGDCFC 9
Db      1 CDCRGDCFC 9

RESULT 29
US-10-304-160-3
; Sequence 3, Application US/10304160
; Publication No. US20030099619A1
; GENERAL INFORMATION:
; APPLICANT: WICKHAM, THOMAS J
; APPLICANT: KOVESDI, IMRE
; APPLICANT: ROELVINK, PETRUS W
; APPLICANT: EINFELD, DAVID
; APPLICANT: BROUGH, DOUGLAS E
; APPLICANT: LIZONOVA, ALENA
; TITLE OF INVENTION: METHOD AND COMPOSITION FOR TARGETING AN ADENOVIRAL VECTOR
; FILE REFERENCE: 220148
; CURRENT APPLICATION NUMBER: US/10/304,160
; CURRENT FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: PCT/US01/17391
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: US 09/631,191
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: US 60/208451
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 3
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-304-160-3

Query Match      100.0%; Score 65; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CDCRGDCFC 9
Db      1 CDCRGDCFC 9

RESULT 30
US-10-264-374-1
; Sequence 1, Application US/10264374
; Publication No. US20030113320A1
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: NGR Receptor and Methods of Identifying Tumor Homing
; TITLE OF INVENTION: Molecules That Home to Angiogenic Vasculature Using
; TITLE OF INVENTION: Same
; FILE REFERENCE: P-LJ 3203
; CURRENT APPLICATION NUMBER: US/10/264,374
; CURRENT FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: US/09/139,802
; PRIOR FILING DATE: 1998-08-25
; PRIOR APPLICATION NUMBER: 08/926,914
; PRIOR FILING DATE: 1997-09-10
; PRIOR APPLICATION NUMBER: 08/710,067
; PRIOR FILING DATE: 1996-09-10
; NUMBER OF SEQ ID NOS: 226
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-264-374-1

Query Match      100.0%; Score 65; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CDCRGDCFC 9
Db      1 CDCRGDCFC 9

RESULT 31
US-10-032-221B-35
; Sequence 35, Application US/10032221B
; Publication No. US20030144481A1
; GENERAL INFORMATION:
; APPLICANT: Kalluri, Raghuram
; TITLE OF INVENTION: ANTI-ANGIOGENIC PROTEINS AND FRAGMENTS AND METHODS OF USE THEREOF
; FILE REFERENCE: 2312/2082B (formerly 1440.1027-016)
; CURRENT APPLICATION NUMBER: US/10/032,221B
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: PCT/US01/00565
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: US 09/625,191
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 09/543,371
; PRIOR FILING DATE: 2000-04-04
; PRIOR APPLICATION NUMBER: US 09/479,118
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/335,224
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: US 60/126,175
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: US 60/089,689
; PRIOR FILING DATE: 1998-06-17
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic blocking peptide
US-10-032-221B-35

Query Match      100.0%; Score 65; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CDCRGDCFC 9
Db      1 CDCRGDCFC 9

RESULT 22
US-10-375-992-1
; Sequence 1, Application US/10375992
; Publication No. US20030152578A1
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
;              Pasqualini, Renata
; TITLE OF INVENTION: Tumor Homing Molecules, Conjugates
;              Derived Therefrom, and Methods of Using Same
; NUMBER OF SEQUENCES: 199
; CORRESPONDENCE ADDRESS:
```

```
; ADDRESSEE: Campbell & Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/375,992
; FILING DATE: 27-Feb-2003
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/926,914
; FILING DATE: 10-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 2725
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: both
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-375-992-1

Query Match      100.0%; Score 65; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CDCRGDCFC 9
Db      1 CDCRGDCFC 9

RESULT 33
US-10-666-696-450
; Sequence 450, Application US/10666696
; Publication No. US20040077022A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-PA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; APPLICANT: GUDAS, JEAN MARIE
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527A
; CURRENT APPLICATION NUMBER: US/10/666,696
; CURRENT FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: US/09/563,286C
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/428,082
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1157
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 450
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: INTEGRIN-BINDING PEPTIDE
US-10-666-696-450
```

```
Query Match      100.0%; Score 65; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDCRGDCFC 9
Db 1 CDCRGDCFC 9

RESULT 34
US-10-666-696-1076
; Sequence 1076, Application US/10666696
; Publication No. US20040077022A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; APPLICANT: GUDAS, JEAN MARIE
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527A
; CURRENT APPLICATION NUMBER: US/10/666,696
; CURRENT FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: US/09/563,286C
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/428,082
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1157
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1076
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: INTEGRIN-BINDING PEPTIDE
US-10-666-696-1076

Query Match      100.0%; Score 65; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDCRGDCFC 9
Db 1 CDCRGDCFC 9

RESULT 35
US-10-653-048-450
; Sequence 450, Application US/10653048
; Publication No. US20040087778A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/653,048
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 450
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: INTEGRIN-BINDING PEPTIDE
```

```
US-10-653-048-450

Query Match      100.0%; Score 65; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDCRGDCFC 9
Db 1 CDCRGDCFC 9

RESULT 36
US-10-653-048-1076
; Sequence 1076, Application US/10653048
; Publication No. US20040087778A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/653,048
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1076
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: INTEGRIN-BINDING PEPTIDE
US-10-653-048-1076

Query Match      100.0%; Score 65; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDCRGDCFC 9
Db 1 CDCRGDCFC 9

RESULT 37
US-10-264-374-1
; Sequence 1, Application US/10264374
; Publication No. US20040096441A9
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: NGR Receptor and Methods of Identifying Tumor Homing
; TITLE OF INVENTION: Molecules That Home to Angiogenic Vasculature Using
; TITLE OF INVENTION: Same
; FILE REFERENCE: P-LJ 3203
; CURRENT APPLICATION NUMBER: US/10/264,374
; CURRENT FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: US/09/139,802
; PRIOR FILING DATE: 1998-08-25
; PRIOR APPLICATION NUMBER: 08/926,914
; PRIOR FILING DATE: 1997-09-10
; PRIOR APPLICATION NUMBER: 08/710,067
; PRIOR FILING DATE: 1996-09-10
; NUMBER OF SEQ ID NOS: 226
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-264-374-1

Query Match      100.0%; Score 65; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CDCRGDCFC 9
         |||||
Db       1 CDCRGDCFC 9

Search completed: July 11, 2004, 10:07:45
Job time : 45 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 11, 2004, 10:00:48 ; Search time 23 Seconds
(without alignments)
20.201 Million cell updates/sec

Title: US-09-734-628-1

Perfect score: 65

Sequence: 1 CDCRGDCFC 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 89883

Minimum DB seq length: 0

Maximum DB seq length: 9

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	65	100.0	9	2	US-08-701-124-3	Sequence 3, Appli
2	65	100.0	9	2	US-08-286-861-16	Sequence 16, Appli
3	65	100.0	9	3	US-09-026-633-1	Sequence 1, Appli
4	65	100.0	9	3	US-09-130-225-3	Sequence 3, Appli
5	65	100.0	9	3	US-09-124-671-33	Sequence 33, Appli
6	65	100.0	9	3	US-09-258-754-211	Sequence 211, App
7	65	100.0	9	3	US-09-138-802-1	Sequence 1, Appli
8	65	100.0	9	3	US-09-042-107-211	Sequence 211, App
9	65	100.0	9	3	US-09-320-424-20	Sequence 20, Appli
10	65	100.0	9	3	US-09-426-680-12	Sequence 12, Appli
11	65	100.0	9	4	US-09-455-061-3	Sequence 3, Appli
12	65	100.0	9	4	US-09-174-943-8	Sequence 8, Appli
13	65	100.0	9	4	US-09-315-127-18	Sequence 18, Appli
14	65	100.0	9	4	US-09-653-786-1	Sequence 1, Appli
15	65	100.0	9	4	US-09-825-563-20	Sequence 20, Appli
16	65	100.0	9	4	US-09-926-914-1	Sequence 1, Appli
17	65	100.0	9	4	US-09-722-250D-211	Sequence 211, App
18	65	100.0	9	4	US-09-969-192-3	Sequence 3, Appli
19	65	100.0	9	4	US-09-428-082B-450	Sequence 450, App
20	65	100.0	9	4	US-09-428-082B-1076	Sequence 1076, App
21	65	100.0	9	4	US-08-660-377A-10	Sequence 10, Appli
22	59	90.8	9	2	US-08-286-861-17	Sequence 17, Appli
23	59	90.8	9	4	US-09-428-082B-451	Sequence 451, App
24	56	86.2	8	3	US-09-026-633-4	Sequence 4, Appli
25	51	78.5	9	2	US-08-701-124-4	Sequence 4, Appli
26	51	78.5	9	2	US-08-286-861-15	Sequence 15, Appli
27	51	78.5	9	3	US-09-130-225-4	Sequence 4, Appli

28 51 78.5 9 4 US-09-455-061-4 Sequence 4, Appli
29 51 78.5 9 4 US-09-989-192-4 Sequence 4, Appli
30 51 78.5 9 4 US-09-428-082B-449 Sequence 449, App
31 49 75.4 9 2 US-08-286-861-18 Sequence 18, Appli
32 49 75.4 9 4 US-09-428-082B-452 Sequence 452, App
33 44 67.7 7 3 US-09-426-680-11 Sequence 11, Appli
34 40 61.5 8 1 US-08-421-702A-22 Sequence 22, Appli
35 40 61.5 8 1 US-08-303-052A-22 Sequence 22, Appli
36 40 61.5 8 1 US-08-421-896A-22 Sequence 22, Appli
37 40 61.5 8 1 US-08-421-897A-22 Sequence 22, Appli
38 40 61.5 8 1 US-08-421-698A-22 Sequence 22, Appli
39 40 61.5 8 2 US-08-421-695A-22 Sequence 22, Appli
40 40 61.5 8 5 PCT-US95-04741-22 Sequence 22, Appli
41 38 58.5 7 2 US-08-286-861-14 Sequence 14, Appli
42 35 53.8 5 1 US-08-212-186A-10 Sequence 10, Appli
43 35 53.8 5 1 US-08-425-238-8 Sequence 8, Appli
44 35 53.8 5 2 US-08-625-695A-10 Sequence 10, Appli
45 35 53.8 5 2 US-08-335-832-42 Sequence 42, Appli

ALIGNMENTS

RESULT 1
US-08-701-124-3
; Sequence 3, Application US/08701124
; Patent No. 5846782
; GENERAL INFORMATION:
; APPLICANT: Wickham, Thomas J.
; APPLICANT: Roelvink, Petrus W.
; APPLICANT: Kovesdi, Imre
; TITLE OF INVENTION: TARGETING ADENOVIRUS WITH USE OF
; TITLE OF INVENTION: CONSTRAINED PEPTIDE MOTIFS
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Voit & Mayer, Ltd.
; STREET: Two Prudential Plaza - 49th Floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/701,124
; FILING DATE: 21-AUG-1996
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-701-124-3

Query Match 100.0%; Score 65; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDCRGDCFC 9
Db 1 CDCRGDCFC 9

RESULT 2
US-08-286-861-16
; Sequence 15, Application US/08286861
; Patent No. 5981478
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki

us-09-734-628-1.closed.ra1

Sun Jul 11 10:16:14 2004

APPLICANT: Koivunen, Erkki
TITLE OF INVENTION: No. 5981478e1 Integrin-Binding Peptides
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,861
FILING DATE: 04-AUG-1994
CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/158,001
FILING DATE: 24-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 9992
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: circular
US-08-286-861-16

Query Match 100.0%; Score 65; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDCRGDCFC 9
Db 1 CDCRGDCFC 9

RESULT 3
US-09-026-633-1
Sequence 1, Application US/09026633
Patent No. 6025328
GENERAL INFORMATION:
APPLICANT: McMorris, Trevor C.
APPLICANT: Kelner, Michael J.
TITLE OF INVENTION: Antitumor agents
FILE REFERENCE: 103.008US1
CURRENT APPLICATION NUMBER: US/09/026,633
CURRENT FILING DATE: 1998-02-20
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Amino acid sequence
US-09-026-633-1

Query Match 100.0%; Score 65; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDCRGDCFC 9
Db 1 CDCRGDCFC 9

RESULT 4
US-09-130-225-3
Sequence 3, Application US/09130225
Patent No. 6057155
GENERAL INFORMATION:
APPLICANT: Wickham, Thomas J.
APPLICANT: Roelvink, Petrus W.
TITLE OF INVENTION: TARGETING ADENOVIRUS WITH USE OF
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza - 49th Floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/130,225

FILING DATE:
PRIOR APPLICATION DATA: US 8-701124
APPLICATION NUMBER: 21-AUG-1996
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-130-225-3

Query Match 100.0%; Score 65; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDCRGDCFC 9
Db 1 CDCRGDCFC 9

RESULT 5
US-09-124-671-33
Sequence 33, Application US/09124671A
Patent No. 6160088
GENERAL INFORMATION:
APPLICANT: Rothman, James
APPLICANT: Mayhew, Mark
APPLICANT: Hoe, Mee
TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
FILE REFERENCE: 31488
CURRENT APPLICATION NUMBER: US/09/124,671A
CURRENT FILING DATE: 1998-07-29
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 33
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: alpha-five integrin binding motif
US-09-124-671-33

Query Match 100.0%; Score 65; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDCRGDCFC 9
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Db 1 CDCRGDCFC 9
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RESULT 6
US-09-258-754-211
; Sequence 211, Application US/09258754
; Patent No. 6174687
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; APPLICANT: Rajotte, Daniel
; TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
; FILE REFERENCE: P-LJ 3443
; CURRENT APPLICATION NUMBER: US/09/258,754
; CURRENT FILING DATE: 1999-02-26
; EARLIER APPLICATION NUMBER: 09/042,107
; EARLIER FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 452
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 211
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-258-754-211

Query Match 100.0%; Score 65; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDCRGDCFC 9
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Db 1 CDCRGDCFC 9
|||||

RESULT 7
US-09-139-802-1
; Sequence 1, Application US/09139802
; Patent No. 6180084
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: NGR Receptor and Methods of Identifying Tumor Homing
; TITLE OF INVENTION: Molecules That Home to Angiogenic Vasculature Using
; FILE REFERENCE: P-LJ 3203
; CURRENT APPLICATION NUMBER: US/09/139,802
; CURRENT FILING DATE: 1998-08-25
; EARLIER APPLICATION NUMBER: 08/926,914
; EARLIER FILING DATE: 1997-09-10
; EARLIER APPLICATION NUMBER: 08/710,067
; EARLIER FILING DATE: 1996-09-10
; NUMBER OF SEQ ID NOS: 226
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-139-802-1

Query Match 100.0%; Score 65; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDCRGDCFC 9
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Db 1 CDCRGDCFC 9
|||||

RESULT 8
US-09-042-107-211
; Sequence 211, Application US/09042107
; Patent No. 6232287
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
; TITLE OF INVENTION: Tissues
; FILE REFERENCE: P-LJ 2892
; CURRENT APPLICATION NUMBER: US/09/042,107
; CURRENT FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 436
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 211
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-042-107-211

Query Match 100.0%; Score 65; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDCRGDCFC 9
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Db 1 CDCRGDCFC 9
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RESULT 9
US-09-320-424-20
; Sequence 20, Application US/09320424
; Patent No. 6284236
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/09/320,424
; CURRENT FILING DATE: 1999-05-26
; EARLIER APPLICATION NUMBER: 09/190,046
; EARLIER FILING DATE: 1998-11-10
; EARLIER APPLICATION NUMBER: 09/048,641
; EARLIER FILING DATE: 1998-03-26
; EARLIER APPLICATION NUMBER: 08/670,354
; EARLIER FILING DATE: 1996-06-25
; EARLIER APPLICATION NUMBER: 08/548,368
; EARLIER FILING DATE: 1995-11-01
; EARLIER APPLICATION NUMBER: 08/496,632
; EARLIER FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: artificial
; OTHER INFORMATION: peptide
US-09-320-424-20

Query Match 100.0%; Score 65; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDCRGDCFC 9

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-455-061-3

Query Match 100.0%; Score 65; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY 1 CDCRGDCFC 9
Db 1 CDCRGDCFC 9

RESULT 12
US-09-174-943-8
; Sequence 8, Application US/09174943
; Patent No. 6420110
; GENERAL INFORMATION:
; APPLICANT: GYURIS, JENO
; APPLICANT: MORRIS, AARON J.
; TITLE OF INVENTION: METHODS AND REAGENTS FOR ISOLATING BIOLOGICALLY ACTIVE
; TITLE OF INVENTION: PEPTIDES
; FILE REFERENCE: MIV-106.01
; CURRENT APPLICATION NUMBER: US/09/174,943
; CURRENT FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: RGD motif
US-09-174-943-8

Query Match 100.0%; Score 65; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY 1 CDCRGDCFC 9
Db 1 CDCRGDCFC 9

RESULT 13
US-09-315-127-18
; Sequence 18, Application US/09315127
; Patent No. 6448390
; GENERAL INFORMATION:
; APPLICANT: The University of Tennessee, c/o Richard Cox
; TITLE OF INVENTION: Stable Envelope Proteins for Retroviral, Viral and
; TITLE OF INVENTION: Liposome Vectors and Use in Gene and Drug Therapy
; FILE REFERENCE: 44137-5023, U. of Tennessee
; CURRENT APPLICATION NUMBER: US/09/315,127
; CURRENT FILING DATE: 1999-05-20
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SEQ. ID NO.
; OTHER INFORMATION: 14, alpha Vbeta3-binding peptide
US-09-315-127-18

Query Match 100.0%; Score 65; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY 1 CDCRGDCFC 9
Db 1 CDCRGDCFC 9

RESULT 10
US-09-426-680-12
; Sequence 12, Application US/09426680
; Patent No. 6287857
; GENERAL INFORMATION:
; APPLICANT: Catherine R. O'Riordan
; APPLICANT: Samuel C. Wadsworth
; TITLE OF INVENTION: Nucleic Acid Delivery Vehicles
; FILE REFERENCE: GA0103UB2
; CURRENT APPLICATION NUMBER: US/09/426,680
; CURRENT FILING DATE: 1999-10-25
; EARLIER APPLICATION NUMBER: PCT/US99/02680
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 9
; TYPE: PRT
; ORGANISM: human
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (0)...(0)
US-09-426-680-12

Query Match 100.0%; Score 65; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY 1 CDCRGDCFC 9
Db 1 CDCRGDCFC 9

RESULT 11
US-09-455-061-3
; Sequence 3, Application US/09455061
; Patent No. 6329190
; GENERAL INFORMATION:
; APPLICANT: Wickham, Thomas J.
; APPLICANT: Roelvink, Petrus W.
; APPLICANT: Kovessi, Imre
; TITLE OF INVENTION: TARGETING ADENOVIRUS WITH USE OF
; TITLE OF INVENTION: CONSTRAINED PEPTIDE MOTIFS
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Voit & Mayer, Ltd.
; STREET: Two Prudential Plaza - 49th Floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/455,061
; FILING DATE: 06-DEC-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 9-130225
; FILING DATE: 06-AUG-1998
; PRIOR APPLICATION NUMBER: US 8-701124
; FILING DATE: 21-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hefner, M. Daniel
; REGISTRATION NUMBER: 41,826
; REFERENCE/DOCKET NUMBER: 203128
; INFORMATION FOR SEQ ID NO: 3:

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Qy 1 CDCRGDCFC 9
Db 1 CDCRGDCFC 9

RESULT 14
US-09-659-786-1
; Sequence 1, Application US/09659786
; Patent No. 6491894
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: NGR Receptor and Methods of Identifying Tumor Homing
; TITLE OF INVENTION: Molecules That Home to Angiogenic Vasculature Using
; TITLE OF INVENTION: Same
; FILE REFERENCE: P-LJ 3203
; CURRENT APPLICATION NUMBER: US/09/659,786
; CURRENT FILING DATE: 2000-09-11
; PRIOR APPLICATION NUMBER: 08/926,914
; PRIOR FILING DATE: 1997-09-10
; PRIOR APPLICATION NUMBER: 08/710,067
; PRIOR FILING DATE: 1996-09-10
; NUMBER OF SEQ ID NOS: 236
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-659-786-1

Query Match 100.0%; Score 65; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDCRGDCFC 9
Db 1 CDCRGDCFC 9

RESULT 15
US-09-825-563-20
; Sequence 20, Application US/09825563
; Patent No. 6521228
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; APPLICANT: Goodwin, Raymond G.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/09/825,563
; CURRENT FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 09/320,424
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: 09/190,046
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 09/048,641
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 08/670,354
; PRIOR FILING DATE: 1996-06-25
; PRIOR APPLICATION NUMBER: 08/548,368
; PRIOR FILING DATE: 1995-11-01
; PRIOR APPLICATION NUMBER: 08/496,632
; PRIOR FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
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; OTHER INFORMATION: Description of Artificial Sequence: artificial
; OTHER INFORMATION: peptide
US-09-825-563-20

Query Match 100.0%; Score 65; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDCRGDCFC 9
Db 1 CDCRGDCFC 9

RESULT 16
US-08-926-914-1
; Sequence 1, Application US/08926914
; Patent No. 6576239
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Tumor Homing Molecules, Conjugates
; TITLE OF INVENTION: Derived Therefrom, and Methods of Using Same
; NUMBER OF SEQUENCES: 199
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/926,914
; FILING DATE: 10-SEP-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 2725
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: both
; MOLECULE TYPE: peptide
US-08-926-914-1

Query Match 100.0%; Score 65; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDCRGDCFC 9
Db 1 CDCRGDCFC 9

RESULT 17
US-09-722-250D-211
; Sequence 211, Application US/09722250D
; Patent No. 6610651
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
; TITLE OF INVENTION: Tissues
; FILE REFERENCE: P-LJ 4514
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; CURRENT APPLICATION NUMBER: US/09/722,250D
; CURRENT FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: US 09/042,107
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 437
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 211
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-722-250D-211

Query Match 100.0%; Score 65; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDCRGDCFC 9
Db 1 CDCRGDCFC 9

RESULT 18
US-09-969-192-3
; Sequence 3, Application US/09969192
; Patent No. 6649407
; GENERAL INFORMATION:
; APPLICANT: WICKHAM, THOMAS J.
; ROELVINK, PETRUS W.
; KOVESDI, IMRE
; TITLE OF INVENTION: TARGETING ADENOVIRUS WITH USE OF
; CORRESPONDENCE ADDRESSES: 80
; ADDRESSEE: Levigig, Voigt & Mayer, Ltd.
; STREET: Two Prudential Plaza - 49th Floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/969,192
; FILING DATE: 01-Oct-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 9-455061
; FILING DATE: 06-DEC-1999
; APPLICATION NUMBER: US 9-130225
; FILING DATE: 06-AUG-1998
; APPLICATION NUMBER: US 8-701124
; FILING DATE: 21-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hefner, M. Daniel
; REGISTRATION NUMBER: 41,826
; REFERENCE/DOCKET NUMBER: 213564
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-969-192-3

Query Match 100.0%; Score 65; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDCRGDCFC 9
Db 1 CDCRGDCFC 9

RESULT 19
US-09-428-082B-450
; Sequence 450, Application US/09428082B
; Patent No. 6660843
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/09/428,082B
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 450
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: INTEGRIN-BINDING PEPTIDE
US-09-428-082B-450

Query Match 100.0%; Score 65; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDCRGDCFC 9
Db 1 CDCRGDCFC 9

RESULT 20
US-09-428-082B-1076
; Sequence 1076, Application US/09428082B
; Patent No. 6660843
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/09/428,082B
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1076
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: INTEGRIN-BINDING PEPTIDE
US-09-428-082B-1076

Query Match 100.0%; Score 65; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDCRGDCFC 9
Db 1 CDCRGDCFC 9

RESULT 21
US-09-660-377A-10
; Sequence 10, Application US/09660377A
; Patent No. 6685914
; GENERAL INFORMATION:
; APPLICANT: Liu, Shuang
; TITLE OF INVENTION: Macrocyclic Chelants For Metallopharmaceuticals
; FILE REFERENCE: EMS-2207
; CURRENT APPLICATION NUMBER: US/09/660,377A
; CURRENT FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/153,512
; PRIOR FILING DATE: 1999-09-13
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(9)
; OTHER INFORMATION: Cyclo
US-09-660-377A-10

Query Match 100.0%; Score 65; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDCRGDCFC 9
|||
Db 1 CDCRGDCFC 9

Search completed: July 11, 2004, 10:06:48
Job time : 23 secs

